



SEQUENCE LISTING

#14/a

(1) GENERAL INFORMATION:

- (i) APPLICANT: Friedman, Jeffrey M.
Lee, Gwo-Hua
Proenca, Ricardo
- (ii) TITLE OF INVENTION: DB, THE RECEPTOR FOR LEPTIN, NUCLEIC
ACIDS ENCODING THE RECEPTOR, AND USES THEREOF
- (iii) NUMBER OF SEQUENCES: 56
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: David A. Jackson, Esq.
 - (B) STREET: 411 Hackensack Ave, Continental Plaza, 4th
Floor
 - (C) CITY: Hackensack
 - (D) STATE: New Jersey
 - (E) COUNTRY: USA
 - (F) ZIP: 07601
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/586,594
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Jackson Esq., David A.
 - (B) REGISTRATION NUMBER: 26,742
 - (C) REFERENCE/DOCKET NUMBER: 600-1-162
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 201-487-5800
 - (B) TELEFAX: 201-343-1684

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2529 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

RECEIVED
JUL 17 1998
GROUP 1800

(vii) IMMEDIATE SOURCE:
(B) CLONE: A15 (OB-Ra)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

| | | | | | | |
|------------|-------------|-------------|------------|------------|-------------|------|
| GGGCTCAGGT | CGGCGTCGTA | CCAGCCGCTG | AAGCGGTTCT | CCAGGTTCCA | GGCGCTCTCG | 60 |
| CCATGCCGGA | TCAGCACCAG | CTTGTAGCTC | GTGCCGAATT | CGGCACGAGG | TTGCTTTGGG | 120 |
| AATGAGCAAG | GTCAAACTG | CTCTGCACTC | ACAGACAACA | CTGAAGGGAA | GAACTGGCT | 180 |
| TCAGTAGTGA | AGGCTTCAGT | TTTTCGCCAG | CTAGGTGTAA | ACTGGGACAT | AGAGTGCTGG | 240 |
| ATGAAAGGGG | ACTTGACATT | ATTCATCTGT | CATATGGAGC | CATTACCTAA | GAACCCCTTC | 300 |
| AAGAATTATG | ACTCTAAGGT | CCATCTTTTA | TATGATCTGC | CTGAAGTCAT | AGATGATTCTG | 360 |
| CCTCTGCCCC | CACTGAAAGA | CAGCTTTCAG | ACTGTCCAAT | GCAACTGCAG | TCTTCGGGGA | 420 |
| TGTGAATGTC | ATGTGCCGGT | ACCCAGAGCC | AAACTCAACT | ACGCTCTTCT | GATGTATTTG | 480 |
| GAAATCACAT | CTGCCGGTGT | GAGTTTTTCAG | TCACCTCTGA | TGTCAGTGCA | GCCCATGCTT | 540 |
| GTTGTGAAAC | CCGATCCACC | CTTAGGTTTG | CATATGGAAG | TCACAGATGA | TGGTAATTTA | 600 |
| AAGATTTCTT | GGGACAGCCA | AACAATGGCA | CCATTTCCGC | TTCAATATCA | GGTGAAATAT | 660 |
| TTAGAGAATT | CTACAATTGT | AAGAGAGGCT | GCTGAAATTG | TCTCAGCTAC | ATCTCTGCTG | 720 |
| GTAGACAGTG | TGCTTCCTGG | ATCTTCATAT | GAGGTCCAGG | TGAGGAGCAA | GAGACTGGAT | 780 |
| GGTTCAGGAG | TCTGGAGTGA | CTGGAGTTCA | CCTCAAGTCT | TTACCACACA | AGATGTTGTG | 840 |
| TATTTTCCAC | CCAAAATTCT | GACTAGTGTT | GGATCGAATG | CTTCTTTTCA | TTGCATCTAC | 900 |
| AAAAACGAAA | ACCAGATTAT | CTCCTCAAAA | CAGATAGTTT | GGTGGAGGAA | TCTAGCTGAG | 960 |
| AAAATCCCTG | AGATACAGTA | CAGCATTGTG | AGTGACCGAG | TTAGCAAAGT | TACCTTCTCC | 1020 |
| AACCTGAAAG | CCACCAGACC | TCGAGGGAAG | TTTACCTATG | ACGCAGTGTA | CTGCTGCAAT | 1080 |
| GAGCAGGCGT | GCCATCACCG | CTATGCTGAA | TTATACGTGA | TCGATGTCAA | TATCAATATA | 1140 |
| TCATGTGAAA | CTGACGGGTA | CTTAACTAAA | ATGACTTGCA | GATGGTCACC | CAGCACAATC | 1200 |
| CAATCACTAG | TGGGAAGCAC | TGTGCAGCTG | AGGTATCACA | GGCGCAGCCT | GTATTGTCCT | 1260 |
| GATAGTCCAT | CTATTCATCC | TACGTCTGAG | CCCAAAAAC | GCGTCTTACA | GAGAGACGGC | 1320 |
| TTTTATGAAT | GTGTTTTTCCA | GCCAATCTTT | CTATTATCTG | GCTATACAAT | GTGGATCAGG | 1380 |
| ATCAACCATT | CTTTAGGTTT | ACTTGACTCG | CCACCAACGT | GTGTCCTTCC | TGACTCCGTA | 1440 |
| GTAAAACAC | TACCTCCATC | TAACGTAAAA | GCAGAGATTA | CTGTAAACAC | TGGATTATTG | 1500 |
| AAAGTATCTT | GGGAAAAGCC | AGTCTTTCCG | GAGAATAACC | TTCAATTCCA | GATTCGATAT | 1560 |

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| GGCTTAAGTG GAAAAGAAAT ACAATGGAAG ACACATGAGG TATTCGATGC AAAGTCAAAG | 1620 |
| TCTGCCAGCC TGCTGGTGTC AGACCTCTGT GCAGTCTATG TGGTCCAGGT TCGCTGCCGG | 1680 |
| CGGTGGATG GACTAGGATA TTGGAGTAAT TGGAGCAGTC CAGCCTATAC GCTTGTCATG | 1740 |
| GATGTAAAAG TTCCTATGAG AGGGCCTGAA TTTTGGAGAA AAATGGATGG GGACGTTACT | 1800 |
| AAAAAGGAGA GAAATGTCAC CTTGCTTTGG AAGCCCCTGA CGAAAAATGA CTCACTGTGT | 1860 |
| AGTGTGAGGA GGTACGTGGT GAAGCATCGT ACTGCCCACA ATGGGACGTG GTCAGAAGAT | 1920 |
| GTGGGAAATC GGACCAATCT CACTTTCCTG TGGACAGAAC CAGCGCACAC TGTTACAGTT | 1980 |
| CTGGCTGTCA ATTCCCTCGG CGCTTCCCTT GTGAATTTTA ACCTTACCTT CTCATGGCCC | 2040 |
| ATGAGTAAAG TGAGTGCTGT GGAGTCACTC AGTGCTTATC CCCTGAGCAG CAGCTGTGTC | 2100 |
| ATCCTTTCCT GGACACTGTC ACCTGATGAT TATAGTCTGT TATATCTGGT TATTGAATGG | 2160 |
| AAGATCCTTA ATGAAGATGA TGGAATGAAG TGGCTTAGAA TTCCCTCGAA TGTAAAAAG | 2220 |
| TTTATATATCC ACGATAATTT TATTCCCATC GAGAAATATC AGTTTAGTCT TTACCCAGTA | 2280 |
| TTTATGGAAG GAGTTGGAAG ACCAAAGATA ATTAATGGTT TCACCAAAGA TGCTATCGAC | 2340 |
| AAGCAGCAGA ATGACGCAGG GCTGTATGTC ATTGTACCCA TAATTATTTT CTCTTGTGTC | 2400 |
| CTACTGCTCG GAACACTGTT AATTTACAC CAGAGAATGA AAAAGTTGTT TTGGGACGAT | 2460 |
| GTTCCAAACC CCAAGAATTG TTCCTGGGCA CAAGGACTGA ATTTCCAAAA GAGAACGGAC | 2520 |
| ACTCTTTGA | 2529 |

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 842 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: OB-Ra

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Gly Leu Arg Ser Ala Ser Tyr Gln Pro Leu Lys Arg Phe Ser Arg Phe

| | | | |
|---|-----|-----|-----|
| 1 | 5 | 10 | 15 |
| Gln Ala Leu Ser Pro Cys Arg Ile Ser Thr Ser Leu Xaa Leu Val Pro | 20 | 25 | 30 |
| Asn Ser Ala Arg Gly Cys Phe Gly Asn Glu Gln Gly Gln Asn Cys Ser | 35 | 40 | 45 |
| Ala Leu Thr Asp Asn Thr Glu Gly Lys Thr Leu Ala Ser Val Val Lys | 50 | 55 | 60 |
| Ala Ser Val Phe Arg Gln Leu Gly Val Asn Trp Asp Ile Glu Cys Trp | 65 | 70 | 75 |
| Met Lys Gly Asp Leu Thr Leu Phe Ile Cys His Met Glu Pro Leu Pro | 85 | 90 | 95 |
| Lys Asn Pro Phe Lys Asn Tyr Asp Ser Lys Val His Leu Leu Tyr Asp | 100 | 105 | 110 |
| Leu Pro Glu Val Ile Asp Asp Ser Pro Leu Pro Pro Leu Lys Asp Ser | 115 | 120 | 125 |
| Phe Gln Thr Val Gln Cys Asn Cys Ser Leu Arg Gly Cys Glu Cys His | 130 | 135 | 140 |
| Val Pro Val Pro Arg Ala Lys Leu Asn Tyr Ala Leu Leu Met Tyr Leu | 145 | 150 | 155 |
| Glu Ile Thr Ser Ala Gly Val Ser Phe Gln Ser Pro Leu Met Ser Leu | 165 | 170 | 175 |
| Gln Pro Met Leu Val Val Lys Pro Asp Pro Pro Leu Gly Leu His Met | 180 | 185 | 190 |
| Glu Val Thr Asp Asp Gly Asn Leu Lys Ile Ser Trp Asp Ser Gln Thr | 195 | 200 | 205 |
| Met Ala Pro Phe Pro Leu Gln Tyr Gln Val Lys Tyr Leu Glu Asn Ser | 210 | 215 | 220 |
| Thr Ile Val Arg Glu Ala Ala Glu Ile Val Ser Ala Thr Ser Leu Leu | 225 | 230 | 235 |
| Val Asp Ser Val Leu Pro Gly Ser Ser Tyr Glu Val Gln Val Arg Ser | 245 | 250 | 255 |
| Lys Arg Leu Asp Gly Ser Gly Val Trp Ser Asp Trp Ser Ser Pro Gln | 260 | 265 | 270 |
| Val Phe Thr Thr Gln Asp Val Val Tyr Phe Pro Pro Lys Ile Leu Thr | 275 | 280 | 285 |
| Ser Val Gly Ser Asn Ala Ser Phe His Cys Ile Tyr Lys Asn Glu Asn | 290 | 295 | 300 |
| Gln Ile Ile Ser Ser Lys Gln Ile Val Trp Trp Arg Asn Leu Ala Glu | 305 | 310 | 315 |
| | | | 320 |

Lys Ile Pro Glu Ile Gln Tyr Ser Ile Val Ser Asp Arg Val Ser Lys
 325 330 335
 Val Thr Phe Ser Asn Leu Lys Ala Thr Arg Pro Arg Gly Lys Phe Thr
 340 345 350
 Tyr Asp Ala Val Tyr Cys Cys Asn Glu Gln Ala Cys His His Arg Tyr
 355 360 365
 Ala Glu Leu Tyr Val Ile Asp Val Asn Ile Asn Ile Ser Cys Glu Thr
 370 375 380
 Asp Gly Tyr Leu Thr Lys Met Thr Cys Arg Trp Ser Pro Ser Thr Ile
 385 390 395 400
 Gln Ser Leu Val Gly Ser Thr Val Gln Leu Arg Tyr His Arg Arg Ser
 405 410 415
 Leu Tyr Cys Pro Asp Ser Pro Ser Ile His Pro Thr Ser Glu Pro Lys
 420 425 430
 Asn Cys Val Leu Gln Arg Asp Gly Phe Tyr Glu Cys Val Phe Gln Pro
 435 440 445
 Ile Phe Leu Leu Ser Gly Tyr Thr Met Trp Ile Arg Ile Asn His Ser
 450 455 460
 Leu Gly Ser Leu Asp Ser Pro Pro Thr Cys Val Leu Pro Asp Ser Val
 465 470 475 480
 Val Lys Pro Leu Pro Pro Ser Asn Val Lys Ala Glu Ile Thr Val Asn
 485 490 495
 Thr Gly Leu Leu Lys Val Ser Trp Glu Lys Pro Val Phe Pro Glu Asn
 500 505 510
 Asn Leu Gln Phe Gln Ile Arg Tyr Gly Leu Ser Gly Lys Glu Ile Gln
 515 520 525
 Trp Lys Thr His Glu Val Phe Asp Ala Lys Ser Lys Ser Ala Ser Leu
 530 535 540
 Leu Val Ser Asp Leu Cys Ala Val Tyr Val Val Gln Val Arg Cys Arg
 545 550 555 560
 Arg Leu Asp Gly Leu Gly Tyr Trp Ser Asn Trp Ser Ser Pro Ala Tyr
 565 570 575
 Thr Leu Val Met Asp Val Lys Val Pro Met Arg Gly Pro Glu Phe Trp
 580 585 590
 Arg Lys Met Asp Gly Asp Val Thr Lys Lys Glu Arg Asn Val Thr Leu
 595 600 605
 Leu Trp Lys Pro Leu Thr Lys Asn Asp Ser Leu Cys Ser Val Arg Arg
 610 615 620

Tyr Val Val Lys His Arg Thr Ala His Asn Gly Thr Trp Ser Glu Asp
 625 630 635 640
 Val Gly Asn Arg Thr Asn Leu Thr Phe Leu Trp Thr Glu Pro Ala His
 645 650 655
 Thr Val Thr Val Leu Ala Val Asn Ser Leu Gly Ala Ser Leu Val Asn
 660 665 670
 Phe Asn Leu Thr Phe Ser Trp Pro Met Ser Lys Val Ser Ala Val Glu
 675 680 685
 Ser Leu Ser Ala Tyr Pro Leu Ser Ser Ser Cys Val Ile Leu Ser Trp
 690 695 700
 Thr Leu Ser Pro Asp Asp Tyr Ser Leu Leu Tyr Leu Val Ile Glu Trp
 705 710 715 720
 Lys Ile Leu Asn Glu Asp Asp Gly Met Lys Trp Leu Arg Ile Pro Ser
 725 730 735
 Asn Val Lys Lys Phe Tyr Ile His Asp Asn Phe Ile Pro Ile Glu Lys
 740 745 750
 Tyr Gln Phe Ser Leu Tyr Pro Val Phe Met Glu Gly Val Gly Lys Pro
 755 760 765
 Lys Ile Ile Asn Gly Phe Thr Lys Asp Ala Ile Asp Lys Gln Gln Asn
 770 775 780
 Asp Ala Gly Leu Tyr Val Ile Val Pro Ile Ile Ile Ser Ser Cys Val
 785 790 795 800
 Leu Leu Leu Gly Thr Leu Leu Ile Ser His Gln Arg Met Lys Lys Leu
 805 810 815
 Phe Trp Asp Asp Val Pro Asn Pro Lys Asn Cys Ser Trp Ala Gln Gly
 820 825 830
 Leu Asn Phe Gln Lys Arg Thr Asp Thr Leu
 835 840

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2848 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: A40 (OB-Rb)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

| | |
|--|------|
| CTCATTGAGA GTGCCAACGG GAAGGCTTAA TTAACCTTTG GAANTGAGTC CGAAGAGTCT | 60 |
| GGAAGTNTGT AAGATGGAAG ATACTATACA AGATACTTCA GAGCTGTACA TTCTTCCAGG | 120 |
| GATGTAGGCT AGCAGTTATT TCATTAGTAT ATGTCTATTT TAGAATGGGA AGAATTAGGA | 180 |
| AGATGAATGG AGCCTGTGTC TTTCAC TACT CTCCCAGGAG GTTCCAGAAT AGCNAAAGTG | 240 |
| TCAGCCAGAA TTCTTGAAGT CATAGACTGG AGTTAGAGAT GAACATAAGC TCATGTTAAG | 300 |
| CCTGGGTTAC TTCTTATCAT CCTTAATTTT GAAAGCTAAG AGGGCCTAAC CATCAAGAAC | 360 |
| GTCTTGAGG AAAGAATGTT TTTAACGCCA TTATTCAGTC AAAGAAATTA AGACTTGAGA | 420 |
| GAAATGCTCA TTTCTTCTCT CATGATGGCT CCTTACACCT TACTTCTACC GTACGATCCA | 480 |
| TGNGGCCCTA CCCACGCAGG ATACATGCAT CTATATGAGA GTGTCTNCCC CTCTTAAC TC | 540 |
| AGAGACTCTT GTTCTAGTCT GTGNTATAAA ATT CAGCTTG TGAAGCTTT CTGAGGGGTT | 600 |
| GGCAGCATTC AATTTTACCT GCAATAGGTA AAGGTAATCT TTTGGGAAGT GAAGAGTGTT | 660 |
| ATTAGACATT TCAGAAAGAA CAAACAGGAT TGGGGCTGCT ATGTGTTCTA CACAGGAATC | 720 |
| TTCCATAACA CAGAATAATT TATGTAGATA GAGACAAGAT GGAAATGCCC AGGGCCCCAA | 780 |
| AATAGCCGCT GTTATTTGTT AACCTTCAAG GTTTTCTGTT TGT TTATCTG TTTCTTGCGC | 840 |
| AGGATCATCT TCCAAGCACA TCCTGGGGGA ACAGTGGCAG AGTCACTCGA GTTCATGAAA | 900 |
| CTATGGTGAC ATCTGAGCTT CCTTG GTTCT TCACAGAACA TAAGCAGTTC CTTTGCTTGC | 960 |
| TTGTTAGATG AGAAAAC TTC TTGTCAGTC TGTCTCTACG ACTAGAATGG AAAGCCTTAC | 1020 |
| TACTTCCTAT GTATTCTTAA TATTTCAAAT GTCCTAATTA TGT TTGGCTT CTCTGTCTTT | 1080 |
| AAGGATTTA GTCTCTGGAT TTGAAGAAAT AAATAAATAA ATAAAGGAAA ACTAATTTTC | 1140 |
| TCGTGCCGGA T GACTGCTAG CTGAGCTCAG GCCTACTGCA TTCTACATTT CGACTCTCTC | 1200 |
| CCTCTTCCCC AGTGCTTTAG CACTGGACTG GGCAGTNCCT GGCCTGGTCT AACTCCTGTT | 1260 |
| TCCTGGTGGG AATGTATAAT AAGAACTCCA TGAGTTCTGG TATAAACACT GTGGTCTGTG | 1320 |
| TGCTAATTAA ATCTNGTGTT TCCTACAGCC CCTGACGAAA AATGACTCAC TGTGTAGTGT | 1380 |
| GAGGAGGTAC GTGGTGAAGC ATCGTACTGC CCACAATGGG ACGTGGTCAG AAGATGTGGG | 1440 |
| AAATCGGACC AATCTCACTT TCCTGTGGAC AGAACCAGCG CACTGTGTTA CAGTTCTGGC | 1500 |
| TGTCAATTCC CTCGGCGCTT CCCTTGTGAA TTTTAACCTT ACCTTCTCAT GGCCCATGAG | 1560 |

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|--|------|
| TAAAGTGAGT GCTGTGGAGT CACTCAGTGC TTATCCCCTG AGCAGCAGCT GTGTCATCCT | 1620 |
| TTCTGGACA CTGTCACCTG ATGATTATAG TCTGTTATAT CTGGTTATTG AATGGAAGAT | 1680 |
| CCTTAATGAA GATGATGGAA TGAAGTGGCT TAGAATTCCC TCGAATGTTA AAAAGTTTAA | 1740 |
| TATCCACGAT AATTTTATTC CCATCGAGAA ATATCAGTTT AGTCTTTACC CAGTATTTAT | 1800 |
| GGAAGGAGTT GGAAAACCAA AGATAATTAA TGGTTTCACC AAAGATGCTA TCGACAAGCA | 1860 |
| GCAGAATGAC GCAGGGCTGT ATGTCATTGT ACCCATAATT ATTTCTCTT GTGTCCTACT | 1920 |
| GCTCGGAACA CTGTTAATTT CACACCAGAG AATGAAAAAG TTGTTTTGGG ACGATGTTCC | 1980 |
| AAACCCCAAG AATTGTTTCCT GGGCACAAGG ACTGAATTTT CAAAAGCCTG AACATTNGA | 2040 |
| GCATCTTTTT ACCAAGCATG CAGAATCAGT GATATTTGGT CCTCTTCTT TGGAGCCTGA | 2100 |
| ACCCATTTCA GAAGAAATCA GTGTCGATAC AGCTTGGAAT AATAAGATG AGATGGTCCC | 2160 |
| AGCAGCTATG GTCTCCCTNC TNNGGACCAC ACCAGACCCT GAAAGCAGTT CTATTTGTNT | 2220 |
| TAGTGACCAG TGTAACAGTG CTAACCTCTC TGGGTCTCAG AGCACCCAGG TAACCTGTGA | 2280 |
| GGATGAGTGT CAGAGACAAC CCTCAGTTAA ATATGCAACT CTGGTCAGCA ACGATAAACT | 2340 |
| AGTGGAAGCT GATGAAGAGC AAGGGTTTAT CCATAGTCCT GTCAGCAACT GCATCTCCAG | 2400 |
| TAATCATTCC CCACTGAGGC AGTCTTTCTC TAGCAGCTCC TGGGAGACAG AGGCCAGAC | 2460 |
| ATTTTTCCTT TTATCAGACC AGCAACCCAC CATGATTTCA CCACAACCTT CATTCCTCGGG | 2520 |
| GTTGGATGAG CTTTTGGAAC TGGAGGGAAG TTTTCTGAA GAAAATCACA GGGAGNAGTC | 2580 |
| TGTCTGTTAT CTAGGAGTCA CCTCCGTCCN CAGAAGAGAG AGTGGTGTGC TTTTGAAGTG | 2640 |
| TGAGGCAGGA ATCCTGTGCA CATTCCCAGC CCAGTGTCTG TTCAGTGACA TCAGGATCCT | 2700 |
| CCAGGAGAGA TGCTCACACT TTGTAGAAAA TAATTTGAGT TTAGGGACCT CTGGTGAGAA | 2760 |
| CTTTGGTCCT AACATGCCCC AATTCCAAAC CTGTTCCACG CACAGTCACA AGATAATGGA | 2820 |
| GAATAAGATG TGTGACTTAA CTGTGTAA | 2848 |

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 581 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:
(B) CLONE: OB-Rb

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Leu | Arg | Asp | Leu | Val | Ser | Gly | Phe | Glu | Glu | Ile | Asn | Lys | Ile | Lys | Glu | |
| 1 | | | 5 | | | | | 10 | | | | | 15 | | | |
| Asn | Phe | Ser | Arg | Ala | Gly | Leu | Leu | Ala | Glu | Leu | Arg | Pro | Thr | Ala | Phe | |
| | | | 20 | | | | | 25 | | | | | 30 | | | |
| Tyr | Ile | Ser | Thr | Leu | Ser | Leu | Phe | Pro | Ser | Ala | Leu | Ala | Leu | Asp | Trp | |
| | | 35 | | | | | 40 | | | | | 45 | | | | |
| Ala | Val | Pro | Gly | Leu | Val | Leu | Leu | Phe | Pro | Gly | Gly | Asn | Val | Glu | Leu | |
| | 50 | | | | | 55 | | | | | 60 | | | | | |
| His | Glu | Phe | Trp | Tyr | Lys | His | Cys | Gly | Leu | Cys | Ala | Asn | Ile | Xaa | Cys | |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 | |
| Phe | Leu | Gln | Pro | Leu | Thr | Lys | Asn | Asp | Ser | Leu | Cys | Ser | Val | Arg | Arg | |
| | | | | 85 | | | | | 90 | | | | | 95 | | |
| Tyr | Val | Val | Lys | His | Arg | Thr | Ala | His | Asn | Gly | Thr | Trp | Ser | Glu | Asp | |
| | | | 100 | | | | | 105 | | | | | | 110 | | |
| Val | Gly | Asn | Arg | Thr | Asn | Leu | Thr | Phe | Leu | Trp | Thr | Glu | Pro | Ala | His | |
| | | 115 | | | | | 120 | | | | | 125 | | | | |
| Thr | Val | Thr | Val | Leu | Ala | Val | Asn | Ser | Leu | Gly | Ala | Ser | Leu | Val | Asn | |
| | | 130 | | | | 135 | | | | | 140 | | | | | |
| Phe | Asn | Leu | Thr | Phe | Ser | Trp | Pro | Met | Ser | Lys | Val | Ser | Ala | Val | Glu | |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 | |
| Ser | Leu | Ser | Ala | Tyr | Pro | Leu | Ser | Ser | Ser | Cys | Val | Ile | Leu | Ser | Trp | |
| | | | | 165 | | | | | 170 | | | | | 175 | | |
| Thr | Leu | Ser | Pro | Asp | Asp | Tyr | Ser | Leu | Leu | Tyr | Leu | Val | Ile | Glu | Trp | |
| | | | 180 | | | | | 185 | | | | | 190 | | | |
| Lys | Ile | Leu | Asn | Glu | Asp | Asp | Gly | Met | Lys | Trp | Leu | Arg | Ile | Pro | Ser | |
| | | 195 | | | | | 200 | | | | | 205 | | | | |
| Asn | Val | Lys | Lys | Phe | Tyr | Ile | His | Asp | Asn | Phe | Ile | Pro | Ile | Glu | Lys | |
| | 210 | | | | | 215 | | | | | 220 | | | | | |
| Tyr | Gln | Phe | Ser | Leu | Tyr | Pro | Val | Phe | Met | Glu | Gly | Val | Gly | Lys | Pro | |
| 225 | | | | | 230 | | | | | 235 | | | | 240 | | |
| Lys | Ile | Ile | Asn | Gly | Phe | Thr | Lys | Asp | Ala | Ile | Asp | Lys | Gln | Gln | Asn | |
| | | | 245 | | | | | | 250 | | | | | 255 | | |
| Asp | Ala | Gly | Leu | Tyr | Val | Ile | Val | Pro | Ile | Ile | Ile | Ser | Ser | Cys | Val | |
| | | | 260 | | | | | 265 | | | | | | 270 | | |

| | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Leu | Leu | Gly | Thr | Leu | Leu | Ile | Ser | His | Gln | Arg | Met | Lys | Lys | Leu | 275 | 280 | 285 |
| Phe | Trp | Asp | Asp | Val | Pro | Asn | Pro | Lys | Asn | Cys | Ser | Trp | Ala | Gln | Gly | 290 | 295 | 300 |
| Leu | Asn | Phe | Gln | Lys | Pro | Glu | Thr | Phe | Glu | Gln | Leu | Phe | Thr | Lys | His | 305 | 310 | 315 |
| Ala | Glu | Ser | Val | Ile | Phe | Gly | Pro | Leu | Leu | Leu | Glu | Pro | Glu | Pro | Ile | 325 | 330 | 335 |
| Ser | Glu | Glu | Ile | Ser | Val | Asp | Thr | Ala | Trp | Lys | Asn | Lys | Asp | Glu | Met | 340 | 345 | 350 |
| Val | Pro | Ala | Ala | Met | Val | Ser | Leu | Leu | Trp | Thr | Thr | Pro | Asp | Pro | Glu | 355 | 360 | 365 |
| Ser | Ser | Ser | Ile | Cys | Ile | Ser | Asp | Gln | Cys | Asn | Ser | Ala | Asn | Phe | Ser | 370 | 375 | 380 |
| Gly | Ser | Gln | Ser | Thr | Gln | Val | Cys | Glu | Asp | Glu | Cys | Gln | Arg | Gln | Pro | 385 | 390 | 395 |
| Ser | Val | Lys | Tyr | Ala | Thr | Leu | Val | Ser | Asn | Asp | Lys | Leu | Val | Glu | Thr | 405 | 410 | 415 |
| Asp | Glu | Glu | Gln | Gly | Phe | Ile | His | Ser | Pro | Val | Ser | Asn | Cys | Ile | Ser | 420 | 425 | 430 |
| Ser | Asn | His | Ser | Pro | Leu | Arg | Gln | Ser | Phe | Ser | Ser | Ser | Ser | Trp | Glu | 435 | 440 | 445 |
| Thr | Glu | Ala | Gln | Thr | Phe | Phe | Leu | Leu | Ser | Asp | Gln | Gln | Pro | Thr | Met | 450 | 455 | 460 |
| Ile | Ser | Pro | Gln | Leu | Ser | Phe | Ser | Gly | Leu | Asp | Glu | Leu | Leu | Glu | Leu | 465 | 470 | 475 |
| Glu | Gly | Ser | Phe | Pro | Glu | Glu | Asn | His | Arg | Glu | Lys | Ser | Val | Cys | Tyr | 485 | 490 | 495 |
| Leu | Gly | Val | Thr | Ser | Val | Asn | Arg | Arg | Glu | Ser | Gly | Val | Leu | Leu | Thr | 500 | 505 | 510 |
| Gly | Glu | Ala | Gly | Ile | Leu | Cys | Thr | Phe | Pro | Ala | Gln | Cys | Leu | Phe | Ser | 515 | 520 | 525 |
| Asp | Ile | Arg | Ile | Leu | Gln | Glu | Arg | Cys | Ser | His | Phe | Val | Glu | Asn | Asn | 530 | 535 | 540 |
| Leu | Ser | Leu | Gly | Thr | Ser | Gly | Glu | Asn | Phe | Gly | Pro | Tyr | Met | Pro | Gln | 545 | 550 | 555 |
| Phe | Gln | Thr | Cys | Ser | Thr | His | Ser | His | Lys | Ile | Met | Glu | Asn | Lys | Met | 565 | 570 | 575 |

Cys Asp Phe Thr Val
580

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 961 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:
(B) CLONE: A6 (OB-Rc)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

| | |
|--|-----|
| TTTAAGGGAT TTAGTCTCTG GATTTGAAGA AATAAATAAA TAAATAAAGG AAAACTAATT | 60 |
| TTCTCGTGCC GGATGACTGC TAGCTGAGCT CAGGCCTACT GCATTCTACA TTTCGACTCT | 120 |
| CTCCCTCTTC CCCAGTGCTT TAGCACTGGA CTGGGCAGTN CCTGGCCTGG TCTAACTCCT | 180 |
| GTTTCCTGGT GGGAAATGTAT AATAAGAACT CCATGAGTTC TGGTATAAAC ACTGTGGTCT | 240 |
| GTGTGCTAAT TAAATCTNGT GTTTCCTACA GCCCCTGACG AAAAATGACT CACTGTGTAG | 300 |
| TGTGAGGAGG TACGTGGTGA AGCATCGTAC TGCCCAACAAT GGGACGTGGT CAGAAGATGT | 360 |
| GGGAAATCGG ACCAATCTCA CTTTCCTGTG GACAGAACCA GCGCACACTG TTACAGTTCT | 420 |
| GGCTGTCAAT TCCCTCGGCG CTTCCCTTGT GAATTTTAAC CTTACCTTCT CATGGCCCAT | 480 |
| GAGTAAAGTG AGTGCTGTGG AGTCACTCAG TGCTTATCCC CTGAGCAGCA GCTGTGTCAT | 540 |
| CCTTTCCTGG ACACTGTCAC CTGATGATTA TAGTCTGTTA TATCTGGTTA TTGAATGGAA | 600 |
| GATCCTTAAT GAAGATGATG GAATGAAGTG GCTTAGAATT CCCTCGAATG TTAAAAAGTT | 660 |
| TTATATCCAC GATAATTTTA TTCCCATCGA GAAATATCAG TTTAGTCTTT ACCCAGTATT | 720 |
| TATGGAAGGA GTTGGAAAAC CAAAGATAAT TAATGGTTTC ACCAAAGATG CTATCGACAA | 780 |
| GCAGCAGAAT GACGCAGGGC TGTATGTCAT TGTACCCATA ATTATTCCT CTTGTGTCCT | 840 |
| ACTGCTCGGA ACACTGTTAA TTTCACACCA GAGAATGAAA AAGTTGTTTT GGGACGATGT | 900 |
| TCCAAACCCC AAGAATTGTT CCTGGGCACA AGGACTGAAT TTCCAAAAGG TCACTGTTTA | 960 |
| A | 961 |

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 319 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: OB-Rc

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Leu | Arg | Asp | Leu | Val | Ser | Gly | Phe | Glu | Glu | Ile | Asn | Lys | Xaa | Ile | Lys | |
| 1 | | | 5 | | | | | 10 | | | | | | 15 | | |
| Glu | Asn | Xaa | Phe | Ser | Arg | Ala | Gly | Xaa | Leu | Leu | Ala | Glu | Leu | Arg | Pro | |
| | | 20 | | | | | 25 | | | | | 30 | | | | |
| Thr | Ala | Phe | Tyr | Ile | Ser | Thr | Leu | Ser | Leu | Phe | Pro | Ser | Ala | Leu | Ala | |
| | | 35 | | | | 40 | | | | | 45 | | | | | |
| Leu | Asp | Trp | Ala | Val | Pro | Gly | Leu | Val | Xaa | Leu | Leu | Phe | Pro | Gly | Gly | |
| | 50 | | | | | 55 | | | | 60 | | | | | | |
| Asn | Val | Xaa | Xaa | Glu | Leu | His | Glu | Phe | Trp | Tyr | Lys | His | Cys | Gly | Leu | |
| 65 | | | | 70 | | | | | 75 | | | | | 80 | | |
| Cys | Ala | Asn | Xaa | Ile | Xaa | Cys | Phe | Leu | Gln | Pro | Leu | Thr | Lys | Asn | Asp | |
| | | | 85 | | | | | 90 | | | | | | 95 | | |
| Ser | Leu | Cys | Ser | Val | Arg | Arg | Tyr | Val | Val | Lys | His | Arg | Thr | Ala | His | |
| | | 100 | | | | | 105 | | | | | | 110 | | | |
| Asn | Gly | Thr | Trp | Ser | Glu | Asp | Val | Gly | Asn | Arg | Thr | Asn | Leu | Thr | Phe | |
| | | 115 | | | | | 120 | | | | | 125 | | | | |
| Leu | Trp | Thr | Glu | Pro | Ala | His | Thr | Val | Thr | Val | Leu | Ala | Val | Asn | Ser | |
| | 130 | | | | | 135 | | | | | 140 | | | | | |
| Leu | Gly | Ala | Ser | Leu | Val | Asn | Phe | Asn | Leu | Thr | Phe | Ser | Trp | Pro | Met | |
| 145 | | | | 150 | | | | | 155 | | | | | 160 | | |
| Ser | Lys | Val | Ser | Ala | Val | Glu | Ser | Leu | Ser | Ala | Tyr | Pro | Leu | Ser | Ser | |
| | | | 165 | | | | | 170 | | | | | | 175 | | |
| Ser | Cys | Val | Ile | Leu | Ser | Trp | Thr | Leu | Ser | Pro | Asp | Asp | Tyr | Ser | Leu | |
| | | 180 | | | | | 185 | | | | | | 190 | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Leu | Tyr | Leu | Val | Ile | Glu | Trp | Lys | Ile | Leu | Asn | Glu | Asp | Asp | Gly | Met | |
| | | 195 | | | | | 200 | | | | | 205 | | | | |
| Lys | Trp | Leu | Arg | Ile | Pro | Ser | Asn | Val | Lys | Lys | Phe | Tyr | Ile | His | Asp | |
| | | 210 | | | | 215 | | | | | 220 | | | | | |
| Asn | Phe | Ile | Pro | Ile | Glu | Lys | Tyr | Gln | Phe | Ser | Leu | Tyr | Pro | Val | Phe | |
| | | 225 | | | 230 | | | | | 235 | | | | | 240 | |
| Met | Glu | Gly | Val | Gly | Lys | Pro | Lys | Ile | Ile | Asn | Gly | Phe | Thr | Lys | Asp | |
| | | | 245 | | | | | | 250 | | | | | 255 | | |
| Ala | Ile | Asp | Lys | Gln | Gln | Asn | Asp | Ala | Gly | Leu | Tyr | Val | Ile | Val | Pro | |
| | | | 260 | | | | | 265 | | | | | 270 | | | |
| Ile | Ile | Ile | Ser | Ser | Cys | Val | Leu | Leu | Leu | Gly | Thr | Leu | Leu | Ile | Ser | |
| | | | 275 | | | | 280 | | | | | 285 | | | | |
| His | Gln | Arg | Met | Lys | Lys | Leu | Phe | Trp | Asp | Asp | Val | Pro | Asn | Pro | Lys | |
| | | 290 | | | | 295 | | | | | 300 | | | | | |
| Asn | Cys | Ser | Trp | Ala | Gln | Gly | Leu | Asn | Phe | Gln | Lys | Val | Thr | Val | | |
| | | 305 | | | 310 | | | | 315 | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2703 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

- (B) CLONE: A8 (OB-Rd)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

| | |
|---|-----|
| ATGATGTGTC AGAAATTCTA TGTGGTTTTG TTACACTGGG AATTTCTTTA TGTGATAGCT | 60 |
| GCACTTAACC TGGCATATCC AATCTCTCCC TGGAAATTTA AGTTGTTTTG TGGACCACCG | 120 |
| AACACAACCG ATGACTCCTT TCTCTCACCT GCTGGAGCCC CAAACAATGC CTCGGCTTTG | 180 |
| AAGGGGGCTT CTGAAGCAAT TGTGAAGCT AAATTTAATT CAAGTGGTAT CTACGTTCTT | 240 |
| GAGTTATCCA AAACAGTCTT CCACTGTTGC TTTGGGAATG AGCAAGGTCA AAACGCTCT | 300 |
| GCACTCACAG ACAACACTGA AGGGAAGACA CTGGCTTCAG TAGTGAAGGC TTCAGTTTTT | 360 |

| | | | | | | |
|-------------|-------------|-------------|-------------|------------|-------------|------|
| CGCCAGCTAG | GTGTAAACTG | GGACATAGAG | TGCTGGATGA | AAGGGGACTT | GACATTATTC | 420 |
| ATCTGTCATA | TGGAGCCATT | ACCTAAGAAC | CCCTTCAAGA | ATTATGACTC | TAAGGTCCAT | 480 |
| CTTTTATATG | ATCTGCCTGA | AGTCATAGAT | GATTCGCCCTC | TGCCCCCACT | GAAAGACAGC | 540 |
| TTTCAGACTG | TCCAATGCAA | CTGCAGTCTT | CGGGGATGTG | AATGTCATGT | GCCGGTACCC | 600 |
| AGAGCCAAAC | TCAACTACGC | TCTTCTGATG | TATTTGGAAA | TCACATCTGC | CGGTGTGAGT | 660 |
| TTTCAGTCAC | CTCTGATGTC | ACTGCAGCCC | ATGCTTGTGTG | TGAAACCCGA | TCCACCCTTA | 720 |
| GGTTTGCATA | TGGAAGTCAC | AGATGATGGT | AATTTAAAAGA | TTTCTTGGGA | CAGCCAAACA | 780 |
| ATGGCACCAT | TTCCGCTTCA | ATATCAGGTG | AAATATTTAG | AGAATTCTAC | AATTGTAAGA | 840 |
| GAGGCTGCTG | AAATTGTCTC | AGCTACATCT | CTGCTGGTAG | ACAGTGTGCT | TCCTGGATCT | 900 |
| TCATATGAGG | TCCAGGTGAG | GAGCAAGAGA | CTGGATGGTT | CAGGAGTCTG | GAGTGACTION | 960 |
| AGTTCACCTC | AAGTCTTTAC | CACACAAGAT | GTTGTGTATT | TTCCACCCAA | AATTCTGACT | 1020 |
| AGTGTGTGGAT | CGAATGCTTC | TTTTTCATTGC | ATCTACAAAA | ACGAAAACCA | GATTATCTCC | 1080 |
| TCAAAACAGA | TAGTTTGGTG | GAGGAATCTA | GCTGAGAAAA | TCCCTGAGAT | ACAGTACAGC | 1140 |
| ATTGTGAGTG | ACCGAGTTAG | CAAAGTTACC | TTCTCCAACC | TGAAAGCCAC | CAGACCTCGA | 1200 |
| GGGAAGTTTA | CCTATGACGC | AGTGTACTGC | TGCAATGAGC | AGGCGTGCCA | TCACCGCTAT | 1260 |
| GCTGAATTAT | ACGTGATCGA | TGTCAATATC | AATATATCAT | GTGAAACTGA | CGGGTACTTA | 1320 |
| ACTAAAATGA | CTTGCAGATG | GTCACCCAGC | ACAATCCAAT | CACTAGTGGG | AAGCACTGTG | 1380 |
| CAGCTGAGGT | ATCACAGGCG | CAGCCTGTAT | TGTCCTGATA | GTCCATCTAT | TCATCCTACG | 1440 |
| TCTGAGCCCA | AAAAC TGCGT | CTTACAGAGA | GACGGCTTTT | ATGAATGTGT | TTTCCAGCCA | 1500 |
| ATCTTTCTAT | TATCTGGCTA | TACAATGTGG | ATCAGGATCA | ACCATTCTTT | AGGTTCACCT | 1560 |
| GACTCGCCAC | CAACGTGTGT | CCTTCCTGAC | TCCGTAGTAA | AACCACTACC | TCCATCTAAC | 1620 |
| GTAAAAGCAG | AGATTACTGT | AAACACTGGA | TTATTGAAAG | TATCTTGGGA | AAAGCCAGTC | 1680 |
| TTTCCGGAGA | ATAACCTTCA | ATTCCAGATT | CGATATGGCT | TAAGTGGA | AGAAATACAA | 1740 |
| TGGAAGACAC | ATGAGGTATT | CGATGCAAAG | TCAAAGTCTG | CCAGCCTGCT | GGTGTGAGAC | 1800 |
| CTCTGTGCAG | TCTATGTGGT | CCAGGTTCGC | TGCCGGCGGT | TGGATGGACT | AGGATATTGG | 1860 |
| AGTAATTGGA | GCAGTCCAGC | CTATACGCTT | GTCATGGATG | TAAAAGTTCC | TATGAGAGGG | 1920 |
| CCTGAATTTT | GGAGAAAAAT | GGATGGGGAC | GTTACTAAAA | AGGAGAGAAA | TGTCACCTTG | 1980 |
| CTTTGGAAGC | CCCTGACGAA | AAATGACTCA | CTGTGTAGTG | TGAGGAGGTA | CGTGGTGAAG | 2040 |
| CATCGTACTG | CCCACAATGG | GACGTGGTCA | GAAGATGTGG | GAAATCGGAC | CAATCTCACT | 2100 |

| | |
|---|------|
| TTCTGTGGA CAGAACCAGC GCACACTGTT ACAGTTCTGG CTGTCAATTC CCTCGGCGCT | 2160 |
| TCCCTTGTGA ATTTTAACCT TACCTTCTCA TGGCCCATGA GTAAAGTGAG TGCTGTGGAG | 2220 |
| TCACTCAGTG CTTATCCCCT GAGCAGCAGC TGTGTCATCC TTTCCTGGAC ACTGTCACCT | 2280 |
| GATGATTATA GTCTGTTATA TCTGGTTATT GAATGGAAGA TCCTTAATGA AGATGATGGA | 2340 |
| ATGAAGTGGC TTAGAATTCC CTCGAATGTT AAAAAGTTTT ATATCCACGA TAATTTTATT | 2400 |
| CCCATCGAGA AATATCAGTT TAGTCTTTAC CCAGTATTTA TGGAAGGAGT TGGAAAACCA | 2460 |
| AAGATAATTA ATGGTTTCAC CAAAGATGCT ATCGACAAGC AGCAGAATGA CGCAGGGCTG | 2520 |
| TATGTCATTG TACCATAAT TATTTCTCT TGTGTCCTAC TGCTCGGAAC ACTGTTAATT | 2580 |
| TCACACCAGA GAATGAAAAA GTTGTTTTGG GACGATGTTT CAAACCCCAA GAATTGTTCC | 2640 |
| TGGGCACAAG GACTGAATTT CAAAAGGAT ATATCTTTAC ATGAAGTTTT TATTTTCAGA | 2700 |
| TAG | 2703 |

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 900 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

- (B) CLONE: OB-Rd

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Met | Cys | Gln | Lys | Phe | Tyr | Val | Val | Leu | Leu | His | Trp | Glu | Phe | Leu |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Tyr | Val | Ile | Ala | Ala | Leu | Asn | Leu | Ala | Tyr | Pro | Ile | Ser | Pro | Trp | Lys |
| | | | 20 | | | | 25 | | | | | | 30 | | |
| Phe | Lys | Leu | Phe | Cys | Gly | Pro | Pro | Asn | Thr | Thr | Asp | Asp | Ser | Phe | Leu |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Ser | Pro | Ala | Gly | Ala | Pro | Asn | Asn | Ala | Ser | Ala | Leu | Lys | Gly | Ala | Ser |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Glu | Ala | Ile | Val | Glu | Ala | Lys | Phe | Asn | Ser | Ser | Gly | Ile | Tyr | Val | Pro |

| | | | | | | |
|---|-----|----|-----|----|-----|-----|
| 65 | | 70 | | 75 | | 80 |
| Glu Leu Ser Lys Thr Val Phe His Cys Cys Phe Gly Asn Glu Gln Gly | 85 | | 90 | | 95 | |
| Gln Asn Cys Ser Ala Leu Thr Asp Asn Thr Glu Gly Lys Thr Leu Ala | 100 | | 105 | | 110 | |
| Ser Val Val Lys Ala Ser Val Phe Arg Gln Leu Gly Val Asn Trp Asp | 115 | | 120 | | 125 | |
| Ile Glu Cys Trp Met Lys Gly Asp Leu Thr Leu Phe Ile Cys His Met | 130 | | 135 | | 140 | |
| Glu Pro Leu Pro Lys Asn Pro Phe Lys Asn Tyr Asp Ser Lys Val His | 145 | | 150 | | 155 | 160 |
| Leu Leu Tyr Asp Leu Pro Glu Val Ile Asp Asp Ser Pro Leu Pro Pro | 165 | | 170 | | | 175 |
| Leu Lys Asp Ser Phe Gln Thr Val Gln Cys Asn Cys Ser Leu Arg Gly | 180 | | 185 | | | 190 |
| Cys Glu Cys His Val Pro Val Pro Arg Ala Lys Leu Asn Tyr Ala Leu | 195 | | 200 | | 205 | |
| Leu Met Tyr Leu Glu Ile Thr Ser Ala Gly Val Ser Phe Gln Ser Pro | 210 | | 215 | | 220 | |
| Leu Met Ser Leu Gln Pro Met Leu Val Val Lys Pro Asp Pro Pro Leu | 225 | | 230 | | 235 | 240 |
| Gly Leu His Met Glu Val Thr Asp Asp Gly Asn Leu Lys Ile Ser Trp | 245 | | 250 | | | 255 |
| Asp Ser Gln Thr Met Ala Pro Phe Pro Leu Gln Tyr Gln Val Lys Tyr | 260 | | 265 | | 270 | |
| Leu Glu Asn Ser Thr Ile Val Arg Glu Ala Ala Glu Ile Val Ser Ala | 275 | | 280 | | 285 | |
| Thr Ser Leu Leu Val Asp Ser Val Leu Pro Gly Ser Ser Tyr Glu Val | 290 | | 295 | | 300 | |
| Gln Val Arg Ser Lys Arg Leu Asp Gly Ser Gly Val Trp Ser Asp Trp | 305 | | 310 | | 315 | 320 |
| Ser Ser Pro Gln Val Phe Thr Thr Gln Asp Val Val Tyr Phe Pro Pro | 325 | | 330 | | | 335 |
| Lys Ile Leu Thr Ser Val Gly Ser Asn Ala Ser Phe His Cys Ile Tyr | 340 | | 345 | | 350 | |
| Lys Asn Glu Asn Gln Ile Ile Ser Ser Lys Gln Ile Val Trp Trp Arg | 355 | | 360 | | 365 | |
| Asn Leu Ala Glu Lys Ile Pro Glu Ile Gln Tyr Ser Ile Val Ser Asp | 370 | | 375 | | 380 | |

| | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| Arg | Val | Ser | Lys | Val | Thr | Phe | Ser | Asn | Leu | Lys | Ala | Thr | Arg | Pro | Arg | | |
| 385 | | | | | 390 | | | | | 395 | | | | | 400 | | |
| Gly | Lys | Phe | Thr | Tyr | Asp | Ala | Val | Tyr | Cys | Cys | Asn | Glu | Gln | Ala | Cys | | |
| | | | | 405 | | | | | 410 | | | | | 415 | | | |
| His | His | Arg | Tyr | Ala | Glu | Leu | Tyr | Val | Ile | Asp | Val | Asn | Ile | Asn | Ile | | |
| | | | 420 | | | | | 425 | | | | | 430 | | | | |
| Ser | Cys | Glu | Thr | Asp | Gly | Tyr | Leu | Thr | Lys | Met | Thr | Cys | Arg | Trp | Ser | | |
| | | 435 | | | | | 440 | | | | | 445 | | | | | |
| Pro | Ser | Thr | Ile | Gln | Ser | Leu | Val | Gly | Ser | Thr | Val | Gln | Leu | Arg | Tyr | | |
| | 450 | | | | | 455 | | | | | 460 | | | | | | |
| His | Arg | Arg | Ser | Leu | Tyr | Cys | Pro | Asp | Ser | Pro | Ser | Ile | His | Pro | Thr | | |
| 465 | | | | 470 | | | | | | 475 | | | | | 480 | | |
| Ser | Glu | Pro | Lys | Asn | Cys | Val | Leu | Gln | Arg | Asp | Gly | Phe | Tyr | Glu | Cys | | |
| | | | 485 | | | | | | 490 | | | | | 495 | | | |
| Val | Phe | Gln | Pro | Ile | Phe | Leu | Leu | Ser | Gly | Tyr | Thr | Met | Trp | Ile | Arg | | |
| | | | 500 | | | | | 505 | | | | | 510 | | | | |
| Ile | Asn | His | Ser | Leu | Gly | Ser | Leu | Asp | Ser | Pro | Pro | Thr | Cys | Val | Leu | | |
| | 515 | | | | | | 520 | | | | | 525 | | | | | |
| Pro | Asp | Ser | Val | Val | Lys | Pro | Leu | Pro | Pro | Ser | Asn | Val | Lys | Ala | Glu | | |
| | 530 | | | | | 535 | | | | | 540 | | | | | | |
| Ile | Thr | Val | Asn | Thr | Gly | Leu | Leu | Lys | Val | Ser | Trp | Glu | Lys | Pro | Val | | |
| 545 | | | | | 550 | | | | 555 | | | | | | 560 | | |
| Phe | Pro | Glu | Asn | Asn | Leu | Gln | Phe | Gln | Ile | Arg | Tyr | Gly | Leu | Ser | Gly | | |
| | | | 565 | | | | | 570 | | | | | | 575 | | | |
| Lys | Glu | Ile | Gln | Trp | Lys | Thr | His | Glu | Val | Phe | Asp | Ala | Lys | Ser | Lys | | |
| | | | 580 | | | | | 585 | | | | | 590 | | | | |
| Ser | Ala | Ser | Leu | Leu | Val | Ser | Asp | Leu | Cys | Ala | Val | Tyr | Val | Val | Gln | | |
| | 595 | | | | | | 600 | | | | | 605 | | | | | |
| Val | Arg | Cys | Arg | Arg | Leu | Asp | Gly | Leu | Gly | Tyr | Trp | Ser | Asn | Trp | Ser | | |
| | 610 | | | | | 615 | | | | | 620 | | | | | | |
| Ser | Pro | Ala | Tyr | Thr | Leu | Val | Met | Asp | Val | Lys | Val | Pro | Met | Arg | Gly | | |
| 625 | | | | | 630 | | | | | 635 | | | | | 640 | | |
| Pro | Glu | Phe | Trp | Arg | Lys | Met | Asp | Gly | Asp | Val | Thr | Lys | Lys | Glu | Arg | | |
| | | | 645 | | | | | | 650 | | | | | 655 | | | |
| Asn | Val | Thr | Leu | Leu | Trp | Lys | Pro | Leu | Thr | Lys | Asn | Asp | Ser | Leu | Cys | | |
| | | | 660 | | | | | 665 | | | | | 670 | | | | |
| Ser | Val | Arg | Arg | Tyr | Val | Val | Lys | His | Arg | Thr | Ala | His | Asn | Gly | Thr | | |
| | | | 675 | | | | 680 | | | | | 685 | | | | | |

| | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Trp | Ser | Glu | Asp | Val | Gly | Asn | Arg | Thr | Asn | Leu | Thr | Phe | Leu | Trp | Thr | 690 | 695 | 700 |
| Glu | Pro | Ala | His | Thr | Val | Thr | Val | Leu | Ala | Val | Asn | Ser | Leu | Gly | Ala | 705 | 710 | 715 |
| Ser | Leu | Val | Asn | Phe | Asn | Leu | Thr | Phe | Ser | Trp | Pro | Met | Ser | Lys | Val | 725 | 730 | 735 |
| Ser | Ala | Val | Glu | Ser | Leu | Ser | Ala | Tyr | Pro | Leu | Ser | Ser | Ser | Cys | Val | 740 | 745 | 750 |
| Ile | Leu | Ser | Trp | Thr | Leu | Ser | Pro | Asp | Asp | Tyr | Ser | Leu | Leu | Tyr | Leu | 755 | 760 | 765 |
| Val | Ile | Glu | Trp | Lys | Ile | Leu | Asn | Glu | Asp | Asp | Gly | Met | Lys | Trp | Leu | 770 | 775 | 780 |
| Arg | Ile | Pro | Ser | Asn | Val | Lys | Lys | Phe | Tyr | Ile | His | Asp | Asn | Phe | Ile | 785 | 790 | 795 |
| Pro | Ile | Glu | Lys | Tyr | Gln | Phe | Ser | Leu | Tyr | Pro | Val | Phe | Met | Glu | Gly | 805 | 810 | 815 |
| Val | Gly | Lys | Pro | Lys | Ile | Ile | Asn | Gly | Phe | Thr | Lys | Asp | Ala | Ile | Asp | 820 | 825 | 830 |
| Lys | Gln | Gln | Asn | Asp | Ala | Gly | Leu | Tyr | Val | Ile | Val | Pro | Ile | Ile | Ile | 835 | 840 | 845 |
| Ser | Ser | Cys | Val | Leu | Leu | Leu | Gly | Thr | Leu | Leu | Ile | Ser | His | Gln | Arg | 850 | 855 | 860 |
| Met | Lys | Lys | Leu | Phe | Trp | Asp | Asp | Val | Pro | Asn | Pro | Lys | Asn | Cys | Ser | 865 | 870 | 875 |
| Trp | Ala | Gln | Gly | Leu | Asn | Phe | Gln | Lys | Asp | Ile | Ser | Leu | His | Glu | Val | 885 | 890 | 895 |
| Phe | Ile | Phe | Arg | | | | | | | | | | | | | 900 | | |

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2461 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: A20 (OB-Re)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

| | | | | | | |
|------------|------------|------------|-------------|-------------|------------|------|
| GAGGAATCGT | TCTGCAAATC | CAGGTGTACA | CCTCTGAAGA | AAGATGATGT | GTCAGAAATT | 60 |
| CTATGTGGTT | TTGTTACACT | GGGAATTTCT | TTATGTGATA | GCTGCACTTA | ACCTGGCATA | 120 |
| TCCAATCTCT | CCCTGGAAAT | TTAAGTTGTT | TTGTGGACCA | CCGAACACAA | CCGATGACTC | 180 |
| CTTTCTCTCA | CCTGCTGGAG | CCCCAAACAA | TGCCCTCGGCT | TTGAAGGGGG | CTTCTGAAGC | 240 |
| AATTGTTGAA | GCTAAATTTA | ATTCAAGTGG | TATCTACGTT | CCTGAGTTAT | CCAAAACAGT | 300 |
| CTTCCACTGT | TGCTTTGGGA | ATGAGCAAGG | TCAAAACTGC | TCTGCACTCA | CAGACAACAC | 360 |
| TGAAGGGAAG | AACTGGCTT | CAGTAGTGAA | GGCTTCAGTT | TTTCGCCAGC | TAGGTGTAAA | 420 |
| CTGGGACATA | GAGTGCTGGA | TGAAAGGGGA | CTTGACATTA | TTCATCTGTC | ATATGGAGCC | 480 |
| ATTACCTAAG | AACCCCTTCA | AGAATTATGA | CTCTAAGGTC | CATCTTTTAT | ATGATCTGCC | 540 |
| TGAAGTCATA | GATGATTGCG | CTCTGCCCCC | ACTGAAAGAC | AGCTTTCAGA | CTGTCCAATG | 600 |
| CAACTGCAGT | CTTCGGGGAT | GTGAATGTCA | TGTGCCGGTA | CCCAGAGCCA | AACTCAACTA | 660 |
| CGCTCTTCTG | ATGTATTTGG | AAATCACATC | TGCCGGTGTG | AGTTTTTCAGT | CACCTCTGAT | 720 |
| GTCAGTGCAG | CCCATGCTTG | TTGTGAAACC | CGATCCACCC | TTAGGTTTGC | ATATGGAAGT | 780 |
| CACAGATGAT | GGTAATTTAA | AGATTTCTTG | GGACAGCCAA | ACAATGGCAC | CATTTCCGCT | 840 |
| TCAATATCAG | GTGAAATATT | TAGAGAATTC | TACAATTGTA | AGAGAGGCTG | CTGAAATTGT | 900 |
| CTCAGCTACA | TCTCTGCTGG | TAGACAGTGT | GCTTCCTGGA | TCTTCATATG | AGGTCCAGGT | 960 |
| GAGGAGCAAG | AGACTGGATG | GTTCAGGAGT | CTGGAGTGAC | TGGAGTTCAC | CTCAAGTCTT | 1020 |
| TACCACACAA | GATGTTGTGT | ATTTTCCACC | CAAAATTCCTG | ACTAGTGTTG | GATCGAATGC | 1080 |
| TTCTTTTCAT | TGCATCTACA | AAAACGAAAA | CCAGATTATC | TCCTCAAAAC | AGATAGTTTG | 1140 |
| GTGGAGGAAT | CTAGCTGAGA | AAATCCCTGA | GATACAGTAC | AGCATTTGTA | GTGACCGAGT | 1200 |
| TAGCAAAGTT | ACCTTCTCCA | ACCTGAAAGC | CACCAGACCT | CGAGGGAAGT | TTACCTATGA | 1260 |
| CGCAGTGTAC | TGCTGCAATG | AGCAGGCGTG | CCATCACCCG | TATGCTGAAT | TATACGTGAT | 1320 |
| CGATGTCAAT | ATCAATATAT | CATGTGAAAC | TGACGGGTAC | TTAACTAAAA | TGACTTGCAG | 1380 |
| ATGGTCACCC | AGCACAATCC | AATCACTAGT | GGGAAGCACT | GTGCAGCTGA | GGTATCACAG | 1440 |
| GCGCAGCCTG | TATTGTCCTG | ATAGTCCATC | TATTCATCCT | ACGTCTGAGC | CCAAAAACTG | 1500 |
| CGTCTTACAG | AGAGACGGCT | TTTATGAATG | TGTTTTCCAG | CCAATCTTTC | TATTATCTGG | 1560 |

| | |
|---|------|
| CTATACAATG TGGATCAGGA TCAACCATTC TTTAGGTTCA CTTGACTCGC CACCAACGTG | 1620 |
| TGTCCTTCCT GACTCCGTAG TAAACCACT ACCTCCATCT AACGTAAAAG CAGAGATTAC | 1680 |
| TGTAAACACT GGATTATTGA AAGTATCTTG GGAAAAGCCA GTCTTTCCGG AGAATAACCT | 1740 |
| TCAATTCCAG ATTCGATATG GCTTAAGTGG AAAAGAAATA CAATGGAAGA CACATGAGGT | 1800 |
| ATTCGATGCA AAGTCAAAGT CTGCCAGCCT GCTGGTGTCA GACCTCTGTG CAGTCTATGT | 1860 |
| GGTCCAGGTT CGCTGCCGGC GGTGATGG ACTAGGATAT TGGAGTAATT GGAGCAGTCC | 1920 |
| AGCCTATACG CTTGTCATGG ATGTAAAAGT TCCTATGAGA GGGCCTGAAT TTTGGAGAAA | 1980 |
| AATGGATGGG GACGTTACTA AAAAGGAGAG AAATGTCACC TTGCTTTGGA AGCCCCTGAC | 2040 |
| GAAAAATGAC TCACTGTGTA GTGTGAGGAG GTACGTGGTG AAGCATCGTA CTGCCCACAA | 2100 |
| TGGGACGTGG TCAGAAGATG TGGGAAATCG GACCAATCTC ACTTTCCTGT GGACAGAACC | 2160 |
| AGCGCACACT GTTACAGTTC TGGCTGTCAA TTCCCTCGGC GCTTCCCTTG TGAATTTTAA | 2220 |
| CCTTACCTTC TCATGGCCCA TGAGTAAAGT GAGTGCTGTG GAGTCACTCA GTGCTTATCC | 2280 |
| CCTGAGCAGC AGCTGTGTCA TCCTTTCCTG GACACTGTCA CCTGATGATT ATAGTCTGTT | 2340 |
| ATATCTGGTT ATTGAATGGA AGATCCTTAA TGAAGATGAT GGAATGAAGT GGCTTAGAAT | 2400 |
| TCCCTCGAAT GTTAAAAAGT TTTATATCCA CGGTATGTGT ACTGTACTTT TCATGGATTA | 2460 |
| G | 2461 |

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 805 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: OB-Re

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

| | | | | | | | | | | | | | | | |
|---|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Met | Cys | Gln | Lys | Phe | Tyr | Val | Val | Leu | Leu | His | Trp | Glu | Phe | Leu |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Tyr Val Ile Ala Ala Leu Asn Leu Ala Tyr Pro Ile Ser Pro Trp Lys | | | | | | | | | | | | | | | |

| 20 | | | | | 25 | | | | | 30 | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Phe | Lys | Leu | Phe | Cys | Gly | Pro | Pro | Asn | Thr | Thr | Asp | Asp | Ser | Phe | Leu |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Ser | Pro | Ala | Gly | Ala | Pro | Asn | Asn | Ala | Ser | Ala | Leu | Lys | Gly | Ala | Ser |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Glu | Ala | Ile | Val | Glu | Ala | Lys | Phe | Asn | Ser | Ser | Gly | Ile | Tyr | Val | Pro |
| 65 | | | | | | 70 | | | | | 75 | | | | 80 |
| Glu | Leu | Ser | Lys | Thr | Val | Phe | His | Cys | Cys | Phe | Gly | Asn | Glu | Gln | Gly |
| | | | | 85 | | | | | 90 | | | | | 95 | |
| Gln | Asn | Cys | Ser | Ala | Leu | Thr | Asp | Asn | Thr | Glu | Gly | Lys | Thr | Leu | Ala |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Ser | Val | Val | Lys | Ala | Ser | Val | Phe | Arg | Gln | Leu | Gly | Val | Asn | Trp | Asp |
| | | | 115 | | | | 120 | | | | | 125 | | | |
| Ile | Glu | Cys | Trp | Met | Lys | Gly | Asp | Leu | Thr | Leu | Phe | Ile | Cys | His | Met |
| | 130 | | | | | 135 | | | | | 140 | | | | |
| Glu | Pro | Leu | Pro | Lys | Asn | Pro | Phe | Lys | Asn | Tyr | Asp | Ser | Lys | Val | His |
| 145 | | | | | | 150 | | | | | 155 | | | | 160 |
| Leu | Leu | Tyr | Asp | Leu | Pro | Glu | Val | Ile | Asp | Asp | Ser | Pro | Leu | Pro | Pro |
| | | | | 165 | | | | | 170 | | | | | 175 | |
| Leu | Lys | Asp | Ser | Phe | Gln | Thr | Val | Gln | Cys | Asn | Cys | Ser | Leu | Arg | Gly |
| | | | 180 | | | | | 185 | | | | | 190 | | |
| Cys | Glu | Cys | His | Val | Pro | Val | Pro | Arg | Ala | Lys | Leu | Asn | Tyr | Ala | Leu |
| | | 195 | | | | | 200 | | | | | 205 | | | |
| Leu | Met | Tyr | Leu | Glu | Ile | Thr | Ser | Ala | Gly | Val | Ser | Phe | Gln | Ser | Pro |
| | 210 | | | | | 215 | | | | | 220 | | | | |
| Leu | Met | Ser | Leu | Gln | Pro | Met | Leu | Val | Val | Lys | Pro | Asp | Pro | Pro | Leu |
| 225 | | | | | | 230 | | | | | 235 | | | | 240 |
| Gly | Leu | His | Met | Glu | Val | Thr | Asp | Asp | Gly | Asn | Leu | Lys | Ile | Ser | Trp |
| | | | | 245 | | | | | 250 | | | | | 255 | |
| Asp | Ser | Gln | Thr | Met | Ala | Pro | Phe | Pro | Leu | Gln | Tyr | Gln | Val | Lys | Tyr |
| | | | 260 | | | | | 265 | | | | | 270 | | |
| Leu | Glu | Asn | Ser | Thr | Ile | Val | Arg | Glu | Ala | Ala | Glu | Ile | Val | Ser | Ala |
| | | 275 | | | | | 280 | | | | | 285 | | | |
| Thr | Ser | Leu | Leu | Val | Asp | Ser | Val | Leu | Pro | Gly | Ser | Ser | Tyr | Glu | Val |
| | | 290 | | | | 295 | | | | | 300 | | | | |
| Gln | Val | Arg | Ser | Lys | Arg | Leu | Asp | Gly | Ser | Gly | Val | Trp | Ser | Asp | Trp |
| 305 | | | | | | 310 | | | | | 315 | | | | 320 |
| Ser | Ser | Pro | Gln | Val | Phe | Thr | Thr | Gln | Asp | Val | Val | Tyr | Phe | Pro | Pro |
| | | | | 325 | | | | | 330 | | | | | 335 | |

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Ile | Leu | Thr | Ser | Val | Gly | Ser | Asn | Ala | Ser | Phe | His | Cys | Ile | Tyr | 340 | 345 | 350 | |
| Lys | Asn | Glu | Asn | Gln | Ile | Ile | Ser | Ser | Lys | Gln | Ile | Val | Trp | Trp | Arg | 355 | 360 | 365 | |
| Asn | Leu | Ala | Glu | Lys | Ile | Pro | Glu | Ile | Gln | Tyr | Ser | Ile | Val | Ser | Asp | 370 | 375 | 380 | |
| Arg | Val | Ser | Lys | Val | Thr | Phe | Ser | Asn | Leu | Lys | Ala | Thr | Arg | Pro | Arg | 385 | 390 | 395 | 400 |
| Gly | Lys | Phe | Thr | Tyr | Asp | Ala | Val | Tyr | Cys | Cys | Asn | Glu | Gln | Ala | Cys | 405 | 410 | 415 | |
| His | His | Arg | Tyr | Ala | Glu | Leu | Tyr | Val | Ile | Asp | Val | Asn | Ile | Asn | Ile | 420 | 425 | 430 | |
| Ser | Cys | Glu | Thr | Asp | Gly | Tyr | Leu | Thr | Lys | Met | Thr | Cys | Arg | Trp | Ser | 435 | 440 | 445 | |
| Pro | Ser | Thr | Ile | Gln | Ser | Leu | Val | Gly | Ser | Thr | Val | Gln | Leu | Arg | Tyr | 450 | 455 | 460 | |
| His | Arg | Arg | Ser | Leu | Tyr | Cys | Pro | Asp | Ser | Pro | Ser | Ile | His | Pro | Thr | 465 | 470 | 475 | 480 |
| Ser | Glu | Pro | Lys | Asn | Cys | Val | Leu | Gln | Arg | Asp | Gly | Phe | Tyr | Glu | Cys | 485 | 490 | 495 | |
| Val | Phe | Gln | Pro | Ile | Phe | Leu | Leu | Ser | Gly | Tyr | Thr | Met | Trp | Ile | Arg | 500 | 505 | 510 | |
| Ile | Asn | His | Ser | Leu | Gly | Ser | Leu | Asp | Ser | Pro | Pro | Thr | Cys | Val | Leu | 515 | 520 | 525 | |
| Pro | Asp | Ser | Val | Val | Lys | Pro | Leu | Pro | Pro | Ser | Asn | Val | Lys | Ala | Glu | 530 | 535 | 540 | |
| Ile | Thr | Val | Asn | Thr | Gly | Leu | Leu | Lys | Val | Ser | Trp | Glu | Lys | Pro | Val | 545 | 550 | 555 | 560 |
| Phe | Pro | Glu | Asn | Asn | Leu | Gln | Phe | Gln | Ile | Arg | Tyr | Gly | Leu | Ser | Gly | 565 | 570 | 575 | |
| Lys | Glu | Ile | Gln | Trp | Lys | Thr | His | Glu | Val | Phe | Asp | Ala | Lys | Ser | Lys | 580 | 585 | 590 | |
| Ser | Ala | Ser | Leu | Leu | Val | Ser | Asp | Leu | Cys | Ala | Val | Tyr | Val | Val | Gln | 595 | 600 | 605 | |
| Val | Arg | Cys | Arg | Arg | Leu | Asp | Gly | Leu | Gly | Tyr | Trp | Ser | Asn | Trp | Ser | 610 | 615 | 620 | |
| Ser | Pro | Ala | Tyr | Thr | Leu | Val | Met | Asp | Val | Lys | Val | Pro | Met | Arg | Gly | 625 | 630 | 635 | 640 |

| | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Glu | Phe | Trp | Arg | Lys | Met | Asp | Gly | Asp | Val | Thr | Lys | Lys | Glu | Arg | 645 | 650 | 655 |
| Asn | Val | Thr | Leu | Leu | Trp | Lys | Pro | Leu | Thr | Lys | Asn | Asp | Ser | Leu | Cys | 660 | 665 | 670 |
| Ser | Val | Arg | Arg | Tyr | Val | Val | Lys | His | Arg | Thr | Ala | His | Asn | Gly | Thr | 675 | 680 | 685 |
| Trp | Ser | Glu | Asp | Val | Gly | Asn | Arg | Thr | Asn | Leu | Thr | Phe | Leu | Trp | Thr | 690 | 695 | 700 |
| Glu | Pro | Ala | His | Thr | Val | Thr | Val | Leu | Ala | Val | Asn | Ser | Leu | Gly | Ala | 705 | 710 | 715 |
| Ser | Leu | Val | Asn | Phe | Asn | Leu | Thr | Phe | Ser | Trp | Pro | Met | Ser | Lys | Val | 725 | 730 | 735 |
| Ser | Ala | Val | Glu | Ser | Leu | Ser | Ala | Tyr | Pro | Leu | Ser | Ser | Ser | Cys | Val | 740 | 745 | 750 |
| Ile | Leu | Ser | Trp | Thr | Leu | Ser | Pro | Asp | Asp | Tyr | Ser | Leu | Leu | Tyr | Leu | 755 | 760 | 765 |
| Val | Ile | Glu | Trp | Lys | Ile | Leu | Asn | Glu | Asp | Asp | Gly | Met | Lys | Trp | Leu | 770 | 775 | 780 |
| Arg | Ile | Pro | Ser | Asn | Val | Lys | Lys | Phe | Tyr | Ile | His | Gly | Met | Cys | Thr | 785 | 790 | 795 |
| Val | Leu | Phe | Met | Asp | | | | | | | | | | | | 805 | | |

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: not relevant
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: C-terminal
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: OB-Ra
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Asn Phe Gln Lys Arg Thr Asp Leu

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: C-terminal

(vii) IMMEDIATE SOURCE:

(B) CLONE: OB-Rb

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Phe | Gln | Lys | Pro | Glu | Thr | Phe | Glu | Gln | Leu | Phe | Thr | Lys | His | Ala | 1 | 5 | 10 | 15 |
| Glu | Ser | Val | Ile | Phe | Gly | Pro | Leu | Leu | Leu | Glu | Pro | Glu | Pro | Ile | Ser | 20 | 25 | 30 | |
| Glu | Glu | Ile | Ser | Val | Asp | Thr | Ala | Trp | Lys | Asn | Lys | Asp | Glu | Met | Val | 35 | 40 | 45 | |
| Pro | Ala | Ala | Met | Val | Ser | Leu | Leu | Trp | Thr | Thr | Pro | Asp | Pro | Glu | Ser | 50 | 55 | 60 | |
| Ser | Ser | Ile | Cys | Ile | Ser | Asp | Gln | Cys | Asn | Ser | Ala | Asn | Phe | Ser | Gly | 65 | 70 | 75 | 80 |
| Ser | Gln | Ser | Thr | Gln | Val | Cys | Glu | Asp | Glu | Cys | Gln | Arg | Gln | Pro | Ser | 85 | 90 | 95 | |
| Val | Lys | Tyr | Ala | Thr | Leu | Val | Ser | Asn | Asp | Lys | Leu | Val | Glu | Thr | Asp | 100 | 105 | 110 | |
| Glu | Glu | Gln | Gly | Phe | Ile | His | Ser | Pro | Val | Ser | Asn | Cys | Ile | Ser | Ser | 115 | 120 | 125 | |
| Asn | His | Ser | Pro | Leu | Arg | Gln | Ser | Phe | Ser | Ser | Ser | Ser | Trp | Glu | Thr | 130 | 135 | 140 | |
| Glu | Ala | Gln | Thr | Phe | Phe | Leu | Leu | Ser | Asp | Gln | Gln | Pro | Thr | Met | Ile | 145 | 150 | 155 | 160 |
| Ser | Pro | Gln | Leu | Ser | Phe | Ser | Gly | Leu | Asp | Glu | Leu | Leu | Glu | Leu | Glu | 165 | 170 | 175 | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Ser | Phe | Pro | Glu | Glu | Asn | His | Arg | Glu | Lys | Ser | Val | Cys | Tyr | Leu |
| | | | 180 | | | | | 185 | | | | | 190 | | |
| Gly | Val | Thr | Ser | Val | Asn | Arg | Arg | Glu | Ser | Gly | Val | Leu | Leu | Thr | Gly |
| | | 195 | | | | | 200 | | | | | 205 | | | |
| Glu | Ala | Gly | Ile | Leu | Cys | Thr | Phe | Pro | Ala | Gln | Cys | Leu | Phe | Ser | Asp |
| | 210 | | | | | 215 | | | | | 220 | | | | |
| Ile | Arg | Ile | Leu | Gln | Glu | Arg | Cys | Ser | His | Phe | Val | Glu | Asn | Asn | Leu |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 |
| Ser | Leu | Gly | Thr | Ser | Gly | Glu | Asn | Phe | Gly | Pro | Tyr | Met | Pro | Gln | Phe |
| | | | 245 | | | | | | 250 | | | | | 255 | |
| Gln | Thr | Cys | Ser | Thr | His | Ser | His | Lys | Ile | Met | Glu | Asn | Lys | Met | Cys |
| | | | 260 | | | | | 265 | | | | | 270 | | |
| Asp | Phe | Thr | Val | | | | | | | | | | | | |
| | | | 275 | | | | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: C-terminal
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: OB-Rc
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

| | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|
| Asn | Phe | Gln | Lys | Val | Thr | Val |
| 1 | | | | 5 | | |

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: not relevant
- (ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: C-terminal

(vii) IMMEDIATE SOURCE:

(B) CLONE: OB-Rd

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

| | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Phe | Gln | Lys | Asp | Ile | Ser | His | Glu | Val | Phe | Ile | Phe | Arg |
| 1 | | | | 5 | | | | | 10 | | | | |

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: C-terminal

(vii) IMMEDIATE SOURCE:

(B) CLONE: OB-Re

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

| | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Phe | Tyr | Ile | His | Gly | Met | Cys | Thr | Val | Leu | Phe | Met | Asp |
| 1 | | | | 5 | | | | | 10 | | | |

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vii) IMMEDIATE SOURCE:

(B) CLONE: OB-Ra/db/db

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Pro Gln Lys Arg Thr Asp Thr Leu
1 5

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vii) IMMEDIATE SOURCE:

(B) CLONE: OB-Rb/wt

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Pro Gln Lys Pro Glu Thr
1 5

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 12 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GATGGAGGGA AA

12

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GATGGAGGTA AA

12

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

ATCTTGGGTT CTCTGAAGAA

20

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GAGATTGTCA GTCACAGCCT C

21

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

ATCTGAATTG GAATCAAATA CAC

23

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

AAATCTGTGA TCCTTCTGAA AC

22

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

ACACTGTTAA TTTCACACCA GAG

23

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

AGTCATTCAA ACCATTAGTT TAGG

24

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

TGGATAAACC CTTGCTCTTC A

21

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

TGAACACAAC AACATAAAGC CC

22

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

AGGCTCCCTC AGGGCCAC

18

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GTGACTGAAT GAAGATGTAA TATAC

25

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

TGTTATATCT GGTATTGAA TGG

23

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CATTAAATGA TTTATTATCA GAATTGC

27

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

| | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Pro | Leu | Pro | Lys | Asn | Pro | Phe | Lys | Asn | Tyr | Asp | Ser | Lys |
| 1 | | | | 5 | | | | | 10 | | | | |

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| His | Arg | Arg | Ser | Leu | Tyr | Cys | Pro | Asp | Ser | Pro | Ser | Ile | His | Pro | Thr |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |

Ser Glu Pro Lys
20

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Gln Arg Met Lys Lys Leu Phe Trp Asp Asp Val Pro Asn Pro Lys Asn
 1 5 10 15

Cys Ser Trp

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 166 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:
 (B) CLONE: 7

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

| | |
|---|-----|
| AGGGNAAGCG CCGAGGGAAT TGACAGCCAG AACTGTAACA GTGTGCGCTG GTTCTGTCCA | 60 |
| CAGGAAAGTG AGATTGGTCC GATTTCACAC ATCTTCTGAC CACGTCCCAT TGTGGGCAGT | 120 |
| ACGATGCTTC ACCACGTACC TCCTCACACT ACACAGTGAG TCATTT | 166 |

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 320 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:
 (B) CLONE: 11

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

| | |
|---|----|
| GGTGAAGCAT CGTACTGCCC ACAATGGGAC GTGGTCAGAA GATGTGGGAA ATCGGACCAA | 60 |
|---|----|

| | |
|---|-----|
| TCTCACTTTC CTGTGGACAG AACCAGCGCA CACTGTTACA GTTCTGGCTG TCAATTCCT | 120 |
| CGGCGCTTCC CTTGTGAATT TTAACCTTAC CTTCTCATGG CCCATGAGTA AAGTGAGTGC | 180 |
| TGTGGAGTCA CTCAGTGCTT ATCCCCTGAG CAGCAGCTGT GTCATCCTTT CCTGGACACT | 240 |
| GTCACCTGAT GATTATAGTC TGTTATATCT GGTATTGAA TGGAAGATCC TTAATGAAGA | 300 |
| TGATGGAATG AAGTGGCTTA | 320 |

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 158 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: 42

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

| | |
|---|-----|
| GATTACTGGA GATGCAGTTG CTGACAGGAC TATGGATAAA CCCTTGCTCT TCATCAGTTT | 60 |
| CCACTAGTTT ATCGTTGCTG ACCAGAGTTG CATATTTAAC TGAGGGTTGT CTCTGACACT | 120 |
| CATCCTCACA GGTACCTGG GTGCTCTGAG ACCCAGAG | 158 |

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 192 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: 46

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

| | |
|---|-----|
| AGAGAGATCC CTGACCCTAG TTAGATCTGT TTTCAGGCTC TGTGTTTCATT TGATGTTTCAG | 60 |
| AAGTCAGCAA GGTTCCTCATA TGTCCTGAGT TAGTAAGATG TCTCAGGGTT CCCCCATCAG | 120 |
| CTAACAACCA CTTTGACATG AGAAGGCAGA AAGTTAAAGA ACACTACTTG GTGTTTTACT | 180 |
| TAAAGATACG AG | 192 |

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: 58

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

| | |
|---|-----|
| AGACTGACAA GGAAGTTTTTC TCATCTAACA AGCAAGCAAA GGAAGTCTT ATGTNCTGTG | 60 |
| ANGAACCAAG GNAGCTCAGA TGTCACCATA GTCATCATGA ACTCGAGTGA CTCTGCCACT | 120 |
| GTCCCCCAG GATGTGCTTG GANGATAATC CTGCGCAAGA AACAGATA | 168 |

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 259 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: S3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

| | |
|---|-----|
| AGAATTATGA CTCTAAGGTC CATCTTTTAT ATGATCTGCC TGAAGTCATA GATGATTTCGC | 60 |
| CTCTGCCCCC ACTGAAAGAC AGNTTTCAGA CTGTCCAATG NAACTGCAGT CTTCGGGGAT | 120 |
| GTGAATGTCA TGTGCCAGTA CCCAGAGCCA AACTCAACTA CGCTCTTCTG ATGTATTTGG | 180 |
| NAATCACATC TGCCGGTGTG AGTTTTTCAGT CACCTCTGAT GTCACCTGCAG CCCATGCTTG | 240 |
| TTGTGAAACC CGATCCACC | 259 |

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: S14

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

| | |
|---|-----|
| CTTCAACAAT TGGTTCAGAA GCCCCCTTCA AAGCCGAGGC ATTGTTTGGG GCTCCAGCAG | 60 |
| GTGAGAGAAA GGAGTCATCG GTTGTGTTCG GTGGTCCACA AAACAACCTA AATTTCCAGG | 120 |
| GAGAGATTGG ATATGCCAGG TTAAGTGCAG CTATCACATA AAGAAATTCC CAGTGTAACA | 180 |
| AAACCACATA GANTTTCTAA CACATCATCT TTCTTCAGAG GTGTACACCT GGATTTGCAG | 240 |
| AACGATTCCT | 250 |

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

CCGAGGGAAT TGACAGCC

18

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CTCACTGTGT AGTGTGAGGA GG

22

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

TCCTGTGGAC AGAACCAGC

19

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

TGACACAGCT GCTGCTCAG

19

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

GGTCTCAGAG CACCCAGGTA

20

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

AGAGAGATCC CTGACCCTAG TT

22

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

AACTTTCTGC CTCCTTCTC ATGTCA

26

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

TTTCTCATCT AACAAGCAAG CA

22

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

ATCTGTTTCT TGCGCAGGAT

20

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

CATTGTTTGG GGCTCCAG

18

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

AATCGTTCTG CAAATCCAGG

20

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

TGAAGTCATA GATGATTCGC C

21

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

GTTCGTACCC GACGTCCTG

20

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 894 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: OB-R

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Met Met Cys Gln Lys Phe Tyr Val Val Leu Leu His Trp Glu Phe Leu
1 5 10 15

Tyr Val Ile Ala Ala Leu Asn Leu Ala Tyr Pro Ile Ser Pro Trp Lys
20 25 30

Phe Lys Leu Phe Cys Gly Pro Pro Asn Thr Thr Asp Asp Ser Phe Leu
 35 40 45
 Ser Pro Ala Gly Ala Pro Asn Asn Ala Ser Ala Leu Lys Gly Ala Ser
 50 55 60
 Glu Ala Ile Val Glu Ala Lys Phe Asn Ser Ser Gly Ile Tyr Val Pro
 65 70 75 80
 Glu Leu Ser Lys Thr Val Phe His Cys Cys Phe Gly Asn Glu Gln Gly
 85 90 95
 Gln Asn Cys Ser Ala Leu Thr Asp Asn Thr Glu Gly Lys Thr Leu Ala
 100 105 110
 Ser Val Val Lys Ala Ser Val Phe Arg Gln Leu Gly Val Asn Trp Asp
 115 120 125
 Ile Glu Cys Trp Met Lys Gly Asp Leu Thr Leu Phe Ile Cys His Met
 130 135 140
 Glu Pro Leu Pro Lys Asn Pro Phe Lys Asn Tyr Asp Ser Lys Val His
 145 150 155 160
 Leu Leu Tyr Asp Leu Pro Glu Val Ile Asp Asp Ser Pro Leu Pro Pro
 165 170 175
 Leu Lys Asp Ser Phe Gln Thr Val Gln Cys Asn Cys Ser Leu Arg Gly
 180 185 190
 Cys Glu Cys His Val Pro Val Pro Arg Ala Lys Leu Asn Tyr Ala Leu
 195 200 205
 Leu Met Tyr Leu Glu Ile Thr Ser Ala Gly Val Ser Phe Gln Ser Pro
 210 215 220
 Leu Met Ser Leu Gln Pro Met Leu Val Val Lys Pro Asp Pro Pro Leu
 225 230 235 240
 Gly Leu His Met Glu Val Thr Asp Asp Gly Asn Leu Lys Ile Ser Trp
 245 250 255
 Asp Ser Gln Thr Met Ala Pro Phe Pro Leu Gln Tyr Gln Val Lys Tyr
 260 265 270
 Leu Glu Asn Ser Thr Ile Val Arg Glu Ala Ala Glu Ile Val Ser Ala
 275 280 285
 Thr Ser Leu Leu Val Asp Ser Val Leu Pro Gly Ser Ser Tyr Glu Val
 290 295 300
 Gln Val Arg Ser Lys Arg Leu Asp Gly Ser Gly Val Trp Ser Asp Trp
 305 310 315 320
 Ser Ser Pro Gln Val Phe Thr Thr Gln Asp Val Val Tyr Phe Pro Pro
 325 330 335
 Lys Ile Leu Thr Ser Val Gly Ser Asn Ala Ser Phe His Cys Ile Tyr

| 340 | | | | | | | | | | 345 | | | | | 350 | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|--|
| Lys | Asn | Glu | Asn | Gln | Ile | Ile | Ser | Ser | Lys | Gln | Ile | Val | Trp | Trp | Arg | | | | |
| 355 | | | | | | | | | | 360 | | | | | 365 | | | | |
| Asn | Leu | Ala | Glu | Lys | Ile | Pro | Glu | Ile | Gln | Tyr | Ser | Ile | Val | Ser | Asp | | | | |
| 370 | | | | | | | | | | 375 | | | | | 380 | | | | |
| Arg | Val | Ser | Lys | Val | Thr | Phe | Ser | Asn | Leu | Lys | Ala | Thr | Arg | Pro | Arg | | | | |
| 385 | | | | | | | | | | 390 | | | | | 395 | | | | |
| Gly | Lys | Phe | Thr | Tyr | Asp | Ala | Val | Tyr | Cys | Cys | Asn | Glu | Gln | Ala | Cys | | | | |
| 405 | | | | | | | | | | 410 | | | | | 415 | | | | |
| His | His | Arg | Tyr | Ala | Glu | Leu | Tyr | Val | Ile | Asp | Val | Asn | Ile | Asn | Ile | | | | |
| 420 | | | | | | | | | | 425 | | | | | 430 | | | | |
| Ser | Cys | Glu | Thr | Asp | Gly | Tyr | Leu | Thr | Lys | Met | Thr | Cys | Arg | Trp | Ser | | | | |
| 435 | | | | | | | | | | 440 | | | | | 445 | | | | |
| Pro | Ser | Thr | Ile | Gln | Ser | Leu | Val | Gly | Ser | Thr | Val | Gln | Leu | Arg | Tyr | | | | |
| 450 | | | | | | | | | | 455 | | | | | 460 | | | | |
| His | Arg | Arg | Ser | Leu | Tyr | Cys | Pro | Asp | Ser | Pro | Ser | Ile | His | Pro | Thr | | | | |
| 465 | | | | | | | | | | 470 | | | | | 475 | | | | |
| Ser | Glu | Pro | Lys | Asn | Cys | Val | Leu | Gln | Arg | Asp | Gly | Phe | Tyr | Glu | Cys | | | | |
| 485 | | | | | | | | | | 490 | | | | | 495 | | | | |
| Val | Phe | Gln | Pro | Ile | Phe | Leu | Leu | Ser | Gly | Tyr | Thr | Met | Trp | Ile | Arg | | | | |
| 500 | | | | | | | | | | 505 | | | | | 510 | | | | |
| Ile | Asn | His | Ser | Leu | Gly | Ser | Leu | Asp | Ser | Pro | Pro | Thr | Cys | Val | Leu | | | | |
| 515 | | | | | | | | | | 520 | | | | | 525 | | | | |
| Pro | Asp | Ser | Val | Val | Lys | Pro | Leu | Pro | Pro | Ser | Asn | Val | Lys | Ala | Glu | | | | |
| 530 | | | | | | | | | | 535 | | | | | 540 | | | | |
| Ile | Thr | Val | Asn | Thr | Gly | Leu | Leu | Lys | Val | Ser | Trp | Glu | Lys | Pro | Val | | | | |
| 545 | | | | | | | | | | 550 | | | | | 555 | | | | |
| Phe | Pro | Glu | Asn | Asn | Leu | Gln | Phe | Gln | Ile | Arg | Tyr | Gly | Leu | Ser | Gly | | | | |
| 565 | | | | | | | | | | 570 | | | | | 575 | | | | |
| Lys | Glu | Ile | Gln | Trp | Lys | Thr | His | Glu | Val | Phe | Asp | Ala | Lys | Ser | Lys | | | | |
| 580 | | | | | | | | | | 585 | | | | | 590 | | | | |
| Ser | Ala | Ser | Leu | Leu | Val | Ser | Asp | Leu | Cys | Ala | Val | Tyr | Val | Val | Gln | | | | |
| 595 | | | | | | | | | | 600 | | | | | 605 | | | | |
| Val | Arg | Cys | Arg | Arg | Leu | Asp | Gly | Leu | Gly | Tyr | Trp | Ser | Asn | Trp | Ser | | | | |
| 610 | | | | | | | | | | 615 | | | | | 620 | | | | |
| Ser | Pro | Ala | Tyr | Thr | Leu | Val | Met | Asp | Val | Lys | Val | Pro | Met | Arg | Gly | | | | |
| 625 | | | | | | | | | | 630 | | | | | 635 | | | | |
| Pro | Glu | Phe | Trp | Arg | Lys | Met | Asp | Gly | Asp | Val | Thr | Lys | Lys | Glu | Arg | | | | |
| 645 | | | | | | | | | | 650 | | | | | 655 | | | | |

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Val | Thr | Leu | Leu | Trp | Lys | Pro | Leu | Thr | Lys | Asn | Asp | Ser | Leu | Cys | 660 | 665 | 670 | |
| Ser | Val | Arg | Arg | Tyr | Val | Val | Lys | His | Arg | Thr | Ala | His | Asn | Gly | Thr | 675 | 680 | 685 | |
| Trp | Ser | Glu | Asp | Val | Gly | Asn | Arg | Thr | Asn | Leu | Thr | Phe | Leu | Trp | Thr | 690 | 695 | 700 | |
| Glu | Pro | Ala | His | Thr | Val | Thr | Val | Leu | Ala | Val | Asn | Ser | Leu | Gly | Ala | 705 | 710 | 715 | 720 |
| Ser | Leu | Val | Asn | Phe | Asn | Leu | Thr | Phe | Ser | Trp | Pro | Met | Ser | Lys | Val | 725 | 730 | 735 | |
| Ser | Ala | Val | Glu | Ser | Leu | Ser | Ala | Tyr | Pro | Leu | Ser | Ser | Ser | Cys | Val | 740 | 745 | 750 | |
| Ile | Leu | Ser | Trp | Thr | Leu | Ser | Pro | Asp | Asp | Tyr | Ser | Leu | Leu | Tyr | Leu | 755 | 760 | 765 | |
| Val | Ile | Glu | Trp | Lys | Ile | Leu | Asn | Glu | Asp | Asp | Gly | Met | Lys | Trp | Leu | 770 | 775 | 780 | |
| Arg | Ile | Pro | Ser | Asn | Val | Lys | Lys | Phe | Tyr | Ile | His | Asp | Asn | Phe | Ile | 785 | 790 | 795 | 800 |
| Pro | Ile | Glu | Lys | Tyr | Gln | Phe | Ser | Leu | Tyr | Pro | Val | Phe | Met | Glu | Gly | 805 | 810 | 815 | |
| Val | Gly | Lys | Pro | Lys | Ile | Ile | Asn | Gly | Phe | Thr | Lys | Asp | Ala | Ile | Asp | 820 | 825 | 830 | |
| Lys | Gln | Gln | Asn | Asp | Ala | Gly | Leu | Tyr | Val | Ile | Val | Pro | Ile | Ile | Ile | 835 | 840 | 845 | |
| Ser | Ser | Cys | Val | Leu | Leu | Leu | Gly | Thr | Leu | Leu | Ile | Ser | His | Gln | Arg | 850 | 855 | 860 | |
| Met | Lys | Lys | Leu | Phe | Trp | Asp | Asp | Val | Pro | Asn | Pro | Lys | Asn | Cys | Ser | 865 | 870 | 875 | 880 |
| Trp | Ala | Gln | Gly | Leu | Asn | Phe | Gln | Lys | Arg | Thr | Asp | Thr | Leu | | | 885 | 890 | | |

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1165 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Ile | Cys | Gln | Lys | Phe | Cys | Val | Val | Leu | Leu | His | Trp | Glu | Phe | Ile | |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | | |
| Tyr | Val | Ile | Thr | Ala | Phe | Asn | Leu | Ser | Tyr | Pro | Ile | Thr | Pro | Trp | Arg | |
| | | | 20 | | | | | 25 | | | | | 30 | | | |
| Phe | Lys | Leu | Ser | Cys | Met | Pro | Pro | Asn | Ser | Thr | Tyr | Asp | Tyr | Phe | Leu | |
| | | 35 | | | | | 40 | | | | | 45 | | | | |
| Leu | Pro | Ala | Gly | Leu | Ser | Lys | Asn | Thr | Ser | Asn | Ser | Asn | Gly | His | Tyr | |
| | 50 | | | | | 55 | | | | | 60 | | | | | |
| Glu | Thr | Ala | Val | Glu | Pro | Lys | Phe | Asn | Ser | Ser | Gly | Thr | His | Phe | Ser | |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 | |
| Asn | Leu | Ser | Lys | Thr | Thr | Phe | His | Cys | Cys | Phe | Arg | Ser | Glu | Gln | Asp | |
| | | | 85 | | | | | | 90 | | | | | 95 | | |
| Arg | Asn | Cys | Ser | Leu | Cys | Ala | Asp | Asn | Ile | Glu | Gly | Lys | Thr | Phe | Val | |
| | | | 100 | | | | | 105 | | | | | | 110 | | |
| Ser | Thr | Val | Asn | Ser | Leu | Val | Phe | Gln | Gln | Ile | Asp | Ala | Asn | Trp | Asn | |
| | | 115 | | | | | 120 | | | | | 125 | | | | |
| Ile | Gln | Cys | Trp | Leu | Lys | Gly | Asp | Leu | Lys | Leu | Phe | Ile | Cys | Tyr | Val | |
| | 130 | | | | | 135 | | | | | 140 | | | | | |
| Glu | Ser | Leu | Phe | Lys | Asn | Leu | Phe | Arg | Asn | Tyr | Asn | Tyr | Lys | Val | His | |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 | |
| Leu | Leu | Tyr | Val | Leu | Pro | Glu | Val | Leu | Glu | Asp | Ser | Pro | Leu | Val | Pro | |
| | | | 165 | | | | | | 170 | | | | | 175 | | |
| Gln | Lys | Gly | Ser | Phe | Gln | Met | Val | His | Cys | Asn | Cys | Ser | Val | His | Glu | |
| | | | 180 | | | | | 185 | | | | | | 190 | | |
| Cys | Cys | Glu | Cys | Leu | Val | Pro | Val | Pro | Thr | Ala | Lys | Leu | Asn | Asp | Thr | |
| | | 195 | | | | | 200 | | | | | 205 | | | | |
| Leu | Leu | Met | Cys | Leu | Lys | Ile | Thr | Ser | Gly | Gly | Val | Ile | Phe | Gln | Ser | |
| | 210 | | | | | 215 | | | | | 220 | | | | | |
| Pro | Leu | Met | Ser | Val | Gln | Pro | Ile | Asn | Met | Val | Lys | Pro | Asp | Pro | Pro | |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 | |
| Leu | Gly | Leu | His | Met | Glu | Ile | Thr | Asp | Asp | Gly | Asn | Leu | Lys | Ile | Ser | |
| | | | 245 | | | | | 250 | | | | | | 255 | | |
| Trp | Ser | Ser | Pro | Pro | Leu | Val | Pro | Phe | Pro | Leu | Gln | Tyr | Gln | Val | Lys | |
| | | | 260 | | | | | 265 | | | | | | 270 | | |
| Tyr | Ser | Glu | Asn | Ser | Thr | Thr | Val | Ile | Arg | Glu | Ala | Asp | Lys | Ile | Val | |
| | | 275 | | | | | 280 | | | | | 285 | | | | |
| Ser | Ala | Thr | Ser | Leu | Leu | Val | Asp | Ser | Ile | Leu | Pro | Gly | Ser | Ser | Tyr | |
| | 290 | | | | | 295 | | | | | 300 | | | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Glu | Val | Gln | Val | Arg | Gly | Lys | Arg | Leu | Asp | Gly | Pro | Gly | Ile | Trp | Ser | |
| 305 | | | | | 310 | | | | | 315 | | | | | 320 | |
| Asp | Trp | Ser | Thr | Pro | Arg | Val | Phe | Thr | Thr | Gln | Asp | Val | Ile | Tyr | Phe | |
| | | | | 325 | | | | | 330 | | | | | 335 | | |
| Pro | Pro | Lys | Ile | Leu | Thr | Ser | Val | Gly | Ser | Asn | Val | Ser | Phe | His | Cys | |
| | | | 340 | | | | | 345 | | | | | 350 | | | |
| Ile | Tyr | Lys | Lys | Glu | Asn | Lys | Ile | Val | Pro | Ser | Lys | Glu | Ile | Val | Trp | |
| | | 355 | | | | | 360 | | | | | 365 | | | | |
| Trp | Met | Asn | Leu | Ala | Glu | Lys | Ile | Pro | Gln | Ser | Gln | Tyr | Asp | Val | Val | |
| | 370 | | | | | 375 | | | | | 380 | | | | | |
| Ser | Asp | His | Val | Ser | Lys | Val | Thr | Phe | Phe | Asn | Leu | Asn | Glu | Thr | Lys | |
| 385 | | | | | 390 | | | | | 395 | | | | | 400 | |
| Pro | Arg | Gly | Lys | Phe | Thr | Tyr | Asp | Ala | Val | Tyr | Cys | Cys | Asn | Glu | His | |
| | | | | 405 | | | | | 410 | | | | | 415 | | |
| Glu | Cys | His | His | Arg | Tyr | Ala | Glu | Leu | Tyr | Val | Ile | Asp | Val | Asn | Ile | |
| | | | 420 | | | | | 425 | | | | | 430 | | | |
| Asn | Ile | Ser | Cys | Glu | Thr | Asp | Gly | Tyr | Leu | Thr | Lys | Met | Thr | Cys | Arg | |
| | | 435 | | | | | 440 | | | | | 445 | | | | |
| Trp | Ser | Thr | Ser | Thr | Ile | Gln | Ser | Leu | Ala | Glu | Ser | Thr | Leu | Gln | Leu | |
| | 450 | | | | | 455 | | | | | 460 | | | | | |
| Arg | Tyr | His | Arg | Ser | Ser | Leu | Tyr | Cys | Ser | Asp | Ile | Pro | Ser | Ile | His | |
| 465 | | | | | 470 | | | | | 475 | | | | | 480 | |
| Pro | Ile | Ser | Glu | Pro | Lys | Asp | Cys | Tyr | Leu | Gln | Ser | Asp | Gly | Phe | Tyr | |
| | | | | 485 | | | | | 490 | | | | | 495 | | |
| Glu | Cys | Ile | Phe | Gln | Pro | Ile | Phe | Leu | Leu | Ser | Gly | Tyr | Thr | Met | Trp | |
| | | | 500 | | | | | 505 | | | | | 510 | | | |
| Ile | Arg | Ile | Asn | His | Ser | Leu | Gly | Ser | Leu | Asp | Ser | Pro | Pro | Thr | Cys | |
| | | 515 | | | | | 520 | | | | | 525 | | | | |
| Val | Leu | Pro | Asp | Ser | Val | Val | Lys | Pro | Leu | Pro | Pro | Ser | Ser | Val | Lys | |
| | 530 | | | | | 535 | | | | | 540 | | | | | |
| Ala | Glu | Ile | Thr | Ile | Asn | Ile | Gly | Leu | Leu | Lys | Ile | Ser | Trp | Glu | Lys | |
| 545 | | | | | 550 | | | | | 555 | | | | 560 | | |
| Pro | Val | Phe | Pro | Glu | Asn | Asn | Leu | Gln | Phe | Gln | Ile | Arg | Tyr | Gly | Leu | |
| | | | | 565 | | | | 570 | | | | | | 575 | | |
| Ser | Gly | Lys | Glu | Val | Gln | Trp | Lys | Met | Tyr | Glu | Val | Tyr | Asp | Ala | Lys | |
| | | | 580 | | | | | 585 | | | | | 590 | | | |
| Ser | Lys | Ser | Val | Ser | Leu | Pro | Val | Pro | Asp | Leu | Cys | Ala | Val | Tyr | Ala | |
| | | 595 | | | | | 600 | | | | | 605 | | | | |
| Val | Gln | Val | Arg | Cys | Lys | Arg | Leu | Asp | Gly | Leu | Gly | Tyr | Trp | Ser | Asn | |
| | 610 | | | | | 615 | | | | | 620 | | | | | |
| Trp | Ser | Asn | Pro | Ala | Tyr | Thr | Val | Val | Met | Asp | Ile | Lys | Val | Pro | Met | |
| 625 | | | | | 630 | | | | | 635 | | | | | 640 | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Arg | Gly | Pro | Glu | Phe | Trp | Arg | Ile | Ile | Asn | Gly | Asp | Thr | Met | Lys | Lys | |
| | | | | 645 | | | | | 650 | | | | | 655 | | |
| Glu | Lys | Asn | Val | Thr | Leu | Leu | Trp | Lys | Pro | Leu | Met | Lys | Asn | Asp | Ser | |
| | | | 660 | | | | | 665 | | | | | 670 | | | |
| Leu | Cys | Ser | Val | Gln | Arg | Tyr | Val | Ile | Asn | His | His | Thr | Ser | Cys | Asn | |
| | | 675 | | | | | 680 | | | | | 685 | | | | |
| Gly | Thr | Trp | Ser | Glu | Asp | Val | Gly | Asn | His | Thr | Lys | Phe | Thr | Phe | Leu | |
| | 690 | | | | | 695 | | | | | 700 | | | | | |
| Trp | Thr | Glu | Gln | Ala | His | Thr | Val | Thr | Val | Leu | Ala | Ile | Asn | Ser | Ile | |
| 705 | | | | | 710 | | | | | 715 | | | | | 720 | |
| Gly | Ala | Ser | Val | Ala | Asn | Phe | Asn | Leu | Thr | Phe | Ser | Trp | Pro | Met | Ser | |
| | | | | 725 | | | | | 730 | | | | | 735 | | |
| Lys | Val | Asn | Ile | Val | Gln | Ser | Leu | Ser | Ala | Tyr | Pro | Leu | Asn | Ser | Ser | |
| | | | 740 | | | | | 745 | | | | | 750 | | | |
| Cys | Val | Ile | Val | Ser | Trp | Ile | Leu | Ser | Pro | Ser | Asp | Tyr | Lys | Leu | Met | |
| | | 755 | | | | | 760 | | | | | 765 | | | | |
| Tyr | Phe | Ile | Ile | Glu | Trp | Lys | Asn | Leu | Asn | Glu | Asp | Gly | Glu | Ile | Lys | |
| | 770 | | | | | 775 | | | | | 780 | | | | | |
| Trp | Leu | Arg | Ile | Ser | Ser | Ser | Val | Lys | Lys | Tyr | Tyr | Ile | His | Asp | His | |
| 785 | | | | | 790 | | | | | 795 | | | | | 800 | |
| Phe | Ile | Pro | Ile | Glu | Lys | Tyr | Gln | Phe | Ser | Leu | Tyr | Pro | Ile | Phe | Met | |
| | | | 805 | | | | | 810 | | | | | | 815 | | |
| Glu | Gly | Val | Gly | Lys | Pro | Lys | Ile | Ile | Asn | Ser | Phe | Thr | Gln | Asp | Asp | |
| | | | 820 | | | | | 825 | | | | | 830 | | | |
| Ile | Glu | Lys | His | Gln | Ser | Asp | Ala | Gly | Leu | Tyr | Val | Ile | Val | Pro | Val | |
| | 835 | | | | | | 840 | | | | | 845 | | | | |
| Ile | Ile | Ser | Ser | Ser | Ile | Leu | Leu | Leu | Gly | Thr | Leu | Leu | Ile | Ser | His | |
| | 850 | | | | | 855 | | | | | 860 | | | | | |
| Gln | Arg | Met | Lys | Lys | Leu | Phe | Trp | Glu | Asp | Val | Pro | Asn | Pro | Lys | Asn | |
| 865 | | | | | 870 | | | | | 875 | | | | | 880 | |
| Cys | Ser | Trp | Ala | Gln | Gly | Leu | Asn | Phe | Gln | Lys | Pro | Glu | Thr | Phe | Glu | |
| | | | | 885 | | | | | 890 | | | | | 895 | | |
| His | Leu | Phe | Ile | Lys | His | Thr | Ala | Ser | Val | Thr | Cys | Gly | Pro | Leu | Leu | |
| | | | 900 | | | | | 905 | | | | | 910 | | | |
| Leu | Glu | Pro | Glu | Thr | Ile | Ser | Glu | Asp | Ile | Ser | Val | Asp | Thr | Ser | Trp | |
| | 915 | | | | | | 920 | | | | | 925 | | | | |
| Lys | Asn | Lys | Asp | Glu | Met | Met | Pro | Thr | Thr | Val | Val | Ser | Leu | Leu | Ser | |
| | 930 | | | | | 935 | | | | | | 940 | | | | |
| Thr | Thr | Asp | Leu | Glu | Lys | Gly | Ser | Val | Cys | Ile | Ser | Asp | Gln | Phe | Asn | |
| 945 | | | | | 950 | | | | | 955 | | | | | 960 | |
| Ser | Val | Asn | Phe | Ser | Glu | Ala | Glu | Gly | Thr | Glu | Val | Thr | Tyr | Glu | Ala | |
| | | | | 965 | | | | | 970 | | | | | 975 | | |

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|------|------|------|
| Glu | Ser | Gln | Arg | Gln | Pro | Phe | Val | Lys | Tyr | Ala | Thr | Leu | Ile | Ser | Asn | 980 | 985 | 990 | |
| Ser | Lys | Pro | Ser | Glu | Thr | Gly | Glu | Glu | Gln | Gly | Leu | Ile | Asn | Ser | Ser | 995 | 1000 | 1005 | |
| Val | Thr | Lys | Cys | Phe | Ser | Ser | Lys | Asn | Ser | Pro | Leu | Lys | Asp | Ser | Phe | 1010 | 1015 | 1020 | |
| Ser | Asn | Ser | Ser | Trp | Glu | Ile | Glu | Ala | Gln | Ala | Phe | Phe | Ile | Leu | Ser | 1025 | 1030 | 1035 | 1040 |
| Asp | Gln | His | Pro | Asn | Ile | Ile | Ser | Pro | His | Leu | Thr | Phe | Ser | Glu | Gly | 1045 | 1050 | 1055 | |
| Leu | Asp | Glu | Leu | Leu | Lys | Leu | Glu | Gly | Asn | Phe | Pro | Glu | Glu | Asn | Asn | 1060 | 1065 | 1070 | |
| Asp | Lys | Lys | Ser | Ile | Tyr | Tyr | Leu | Gly | Val | Thr | Ser | Ile | Lys | Lys | Arg | 1075 | 1080 | 1085 | |
| Glu | Ser | Gly | Val | Leu | Leu | Thr | Asp | Lys | Ser | Arg | Val | Ser | Cys | Pro | Phe | 1090 | 1095 | 1100 | |
| Pro | Ala | Pro | Cys | Leu | Phe | Thr | Asp | Ile | Arg | Val | Leu | Gln | Asp | Ser | Cys | 1105 | 1110 | 1115 | 1120 |
| Ser | His | Phe | Val | Glu | Asn | Asn | Ile | Asn | Leu | Gly | Thr | Ser | Ser | Lys | Lys | 1125 | 1130 | 1135 | |
| Thr | Phe | Ala | Ser | Tyr | Met | Pro | Gln | Phe | Gln | Thr | Cys | Ser | Thr | Gln | Thr | 1140 | 1145 | 1150 | |
| His | Lys | Ile | Met | Glu | Asn | Lys | Met | Cys | Asp | Leu | Thr | Val | | | | 1155 | 1160 | 1165 | |